

FIGURE 1

ACTGCACCTCGGTTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGA
CCCACGCGTCCGGGCCGGAGCAGCACGCCGCAGGACCTGGAGCTCCGGCTCGCTTCCCG
CAGCGCTACCCGCCATGCGCCTGCCGCCGGCGCTGGGCTCCTGCCGCTTGCTG
CTGCTGCCGCCGCCGGAGGCCAAGAAGCCGACGCCCTGCCACC GGTCGCCGGGGCT
GGTGGACAAGTTAACCAAGGGATGGTGGACACCGCAAAGAAGAACTTGGCGGGAAACA
CGGCTTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCCCTGCTGGAGATC
CTGGAGGGCTGTGCAGAGCAGCGACTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA
GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTGAGTGGTTT
GTGTGAAGACACTGAAAGTGTGCTGCTCCAGGAACCTACGGTCCGACTGTCTCGCATGC
CAGGGCGGATCCCAGAGGCCCTGCAGCGGAATGCCACTGCAGCGAGATGGAGCAGACA
GGGCGACGGGTCTGCCGGTGCACATGGGTACCAGGGCCGCTGTGCACTGACTGCATGG
ACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATTGCACAGCCTGTGACGAGTCC
TGCAAGACGTGCTCGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGTGGCTGGGTGCT
GGACGAGGGCGCTGTGGATGTGGACGAGTGTGCGGCCGAGCCCTCCCTGCAGCGCTG
CGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTG
GGCTGCACAGGGGAAGGCCAGGAAACTGTAAAGAGTGTATCTCTGGCTACCGAGGGAGCA
CGGACAGTGTGCAGATGTGGACGAGTGCTCACTAGCAGAAAAACCTGTGTGAGGAAAAACG
AAAATGCTACAATACTCCAGGGAGCTACGTCTGTGTGTCCTGACGGCTTCGAAGAACG
GAAGATGCCTGTGTGCCGCCAGAGGCTGAAGCCACAGAAGGAGAAAGCCGACACAGCT
GCCCTCCCGGAAGACCTGTAATGTGCCGGACTTACCCTTAAATTATTCAAGGATGTCC
CGTGGAAAATGTGGCCCTGAGGATGCCGTCTGCAGTGGACAGCGGCCGGAGAGGCTGC
CTGCTCTCTAACGGTTGATTCTCATTGTCCTTAAACAGCTGCATTCTGGTTGTCTTA
AACAGACTTGTATATTTGATACTACAGTTCTTGTAAATAAAATTGACCATTGTAGGTAATCAGG
AGGAAAAAAAAGGGCGGCCGCGACTCTAGAGTCGACCTGCAGAACG
TTGGCCGCCATGGCCAACCTGTTATTGCAGCTTATAATGGTTACAAATAAGCAATAGCA
TCACAAATTTCACAAATAAGCATTTCAGCTGCTAGTTGTGGTTGTCCAAACTC
ATCAATGTATCTTATCATGTCTGGATCGGAATTAAATTGCCGCAGCACCATGGCCTGAAAT
AACCTCTGAAAGAGGAACCTGGTTAGGTACCTCTGAGGCGAAAGAACCAAGCTGTGGAATG
TGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAGCATGC
ATCTCAATTAGTCAGCAACCCAGTTT

FIGURE 2

><subunit 1 of 1, 353 aa, 0 stop

><MW: 38192, pI: 4.53, NX(S/T): 2

MRLPRRAALGLLPLLLLPPAPEAAKKPTPCCHRGRGLVDKFNQGMVDTAKKNFGGGNTAEEKTLSKYESSEIRL
LEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFCVKTLKVCCSPGTYGPDCLACQGGSQRPCSG
NGHCSDGSRQGDGSCRCHMGYQGPLCTDCMDGYFSSLRNEHTSICTACDESCKTCGSLTNRDCGECEVGVLDE
GACVDVDECAAEPPPCSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDEC SLAEKT
CVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEEATEGESPTQLPSREDL

Signal peptide:

amino acids 1-24

N-glycosylation sites.

amino acids 190-194 and 251-255

Glycosaminoglycan attachment sites.

amino acids 149-153 and 155-159

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 26-30

Casein kinase II phosphorylation sites.

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343
and 349-353

Tyrosine kinase phosphorylation site.

amino acids 303-310

N-myristoylation sites.

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and
313-319

Aspartic acid and asparagine hydroxylation site.

amino acids 308-320

EGF-like domain cysteine pattern signature.

amino acids 166-178

Leucine zipper pattern.

amino acids 94-116

FIGURE 3

CAGGTCCAAC TGCACCTCGGTTCTATCGATTGAATTCCCCGGGATCCTCTAGAGATCCCTC
GACCTCGACCCAC CGCGTCCGCCAGGCCGGAGGCAGCGCCCAGCGTCTAAACGGGAACA
GCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGTATCTGACGGCGCAGGTTGCGTAGGTGCG
GCACGAGGAGTTTCCCGCAGCGAGGAGGTCTGAGCAGCAGCAGGGCCGGAGGAGCGCCCTTC
CCTGCCGCCGCGCTCGGCTCTGGAGCATCCTCTGTGCCTGCTGGCACTGCAGGGCGGAGGC
CGGGCCGCCGCAGGAGGAGAGCCTGTACCTATGGATCGATGCTCACCAGGCAAGAGTACTCA
TAGGATTGAGAAGATATCCTGATTGTT CAGAGGGAAAATGGCACCTTTACACATGAT
TTCAGAAAAGCGCAACAGAGAACGCCAGCTATTCCATGTCAATATCCATTCCATGAATTTCAC
CTGGCAAGCTGCAGGGCAGGCAGAATACTTCTATGAATT CCTGTCCTGCGCTCCCTGGATA
AAGGCATCATGGCAGATCCAACCGTCAATGTCCCTCTGCTGGAACAGTGCCCTCACAAGGCA
TCAGTTGTTCAAGTTGGTTCCATGTCTGGAAAACAGGATGGGTGGCAGCATTGAAAGT
GGATGTGATTGTTATGAATTCTGAAGGCAACACCATTCTCAAACACCTCAAAATGCTATCT
TCTTAAAACATGTCAACAAGCTGAGTGCCAGGGCGGCTGCGAAATGGAGGCTTTGTAAT
GAAAGACGCATCTGCAGTGTCTGATGGGTTCCACGGACCTCACTGTGAGAAAGCCCTTG
TACCCCACGATGTATGAATGGTGGACTTTGTGACTCCTGGTTCTGCATCTGCCACCTG
GATTCTATGGAGTGAACTGTGACAAAGCAAAC TGCTCAACCACCTGCTTTAATGGAGGGACC
TGTTTCTACCCCTGGAAAATGTATTTGCCCTCCAGGACTAGAGGGAGAGCAGTGTGAAATCAG
CAAATGCCACAACCGTCAATGGAGGTAAATGCATTGGAAAAGCAAATGTAAGTGT
CCAAAGGTTACCAGGGAGACCTCTGTTCAAAGCCTGCTGCGAGCCTGGCTGGTGACAT
GGAACCTGCCATGAACCCAACAAATGCCATGTCAAGAAGGTTGGCATGGAAGACACTGCAA
TAAAAGGTACGAAGCCAGCCTCATACATGCCCTGAGGCCAGCGGCCAGCTCAGGCAGC
ACACGCCCTCACTTAAAAGGCCGAGGAGCGGGGATCCACCTGAATCCAATTACATCTGG
TGAACTCCGACATCTGAAACGTTAAGTTACACCAAGTTACAGCATTGCTTGTAAACCTTCA
TGTGTTGAATGTTCAAATAATGTTCACTTAAGAATACTGGCCTGAAATTATTTAGCT
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CATGATGGTATAGATTCTTGTTCAGTGTGAGTTGGCAGATATTTCAAATTACAATGCATTATGGT
TCAGGTTAAAATTTCAGTGTGAGTTGGCAGATATTTCAAATTACAATGCATTATGGT
GTCTGGGGGGCAGGGGAACATCAGAAAGGTTAAATTGGGCAAAATCGTAAGTCACAAGAAT
TTGGATGGTGAGTTAATGTTGAAGTTACAGCATTGCTTGTCAAGATTTATTGTCAATTG
GTTTGTACATTAAAAATTGCTCTTAATTAAACTCTCAATACAATATATTGACC
TTACCAATTCCAGAGATTCACTGAGGTTAAATTACACTGTGGTAGTGGCATT
AAACAATATAATATTCTAAACACAATGAAATAGGGAATATAATGTATGAACCTTGCAT
TGGCTGAAGCAATATAATATTGTAACAAAACACAGCTCTTACCTAATAAACATT
ACTGTTGTATGTATAAAATAAGGTGCTGCTTAGTTTTGGAAAAA
AAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGTCGACCTGCAGAAGCTTGGC
CGCCATGGCCCAACTTGTATTGCAGCTTATAATG

FIGURE 4

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094
><subunit 1 of 1, 379 aa, 0 stop
><MW: 41528, pI: 7.97, NX(S/T): 2
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GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPGGC
RNNGFCNERRICECPDGFHGPCKEAKLCPRCMNGLCVTPGFCICPPGFYGVNCDKANCST
TCFNNGTCFYPGKCICPPGLEGEQCEISKCPQPCRNGGKICGSKCKCSKGYQGDLCSPVC
EPGCGAHTCHePNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAERRDP
PESNYIW
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Signal peptide:

amino acids 1-28

N-glycosylation site.

amino acids 88-92, 245-249

Casein kinase II phosphorylation site.

amino acids 319-323

Tyrosine kinase phosphorylation site.

amino acids 370-378

N-myristoylation sites.

amino acids 184-190, 185-191, 189-195, 315-321

ATP/GTP-binding site motif A (P-loop).

amino acids 285-293

EGF-like domain cysteine pattern signature.

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

FIGURE 5

CGGACGCGTGGCGTCGGCGGTGCAGAGCCAGGAGGCCAGGAGGCCACCATGTGGCGATGTCCACTGGGCTAC
CCCCAGCCCACACCTCACCAGGGCCCAGGAGGCCACCATGTGGCGATGTCCACTGGGCTAC
TGCTGTTGCTGCCGCTGGCTGGCCACTTGGCTCTGGGTGCCAGCAGGGTCTGGGCCGG
GAGCTAGCACCGGGCTGCACCTGCAGGGCATCCGGGACGCCGGAGGCCGGTACTGCCAGGA
GCAGGACCTGTGCTGCCGCGCGTGCAGACTGTGCCCTGCCCTACCTGGCGCCATCT
GTTACTGTGACCTCTCTGCAACCGCACGGTCTCCGACTGCTGCCCTGACTTCTGGGACTTC
TGCCTCGGCGTGCCACCCCCCTTCCCCGATCCAAGGATGTATGCATGGAGGTCTGATCTA
TCCAGTCTTGGAACGTACTGGGACAACGTAACTGTAACCGTTGCACCTGCCAGGAGAACAGGCAGT
GGCATGGTGGATCCAGACATGATCAAAGCCATCAACCAGGGCAACTATGGCTGGCAGGCTGG
GAACCACAGGCCCTCTGGGCATGACCTGGTGAGGGCATTGCTACCGCTGGCACCA
TCCGCCATCTCCTCGGTATGAACATGCATGAAATTATAACAGTGCTGAACCCAGGGAG
GTGCTTCCCACAGCCTCGAGGCCTCTGAGAAGTGGCCAACCTGATTGATGAGCCTCTTGA
CCAAGGCAACTGTGCAAGGCTCTGGGCCTCTCCACAGCAGCTGTGGCATCCGATCGTGTCT
CAATCCATTCTCTGGGACACATGACGCCCTGTCTGCCCCAGAACCTGCTGTCTTGAC
ACCCACCAGCAGCAGGGCTGCCCGGTGGCGTCTCGATGGTGCCTGGTGGTCTGCC
CCGAGGGGTGGTGTCTGACCACTGCTACCCCTCTGGGCCTGAAACGAGACGAGGCTGGC
CTGCCCCCTGTATGATGCAAGCCAGGACATGGTCGGGCAAGGCCAGGCCACTGCC
CACTGCCCAACAGCTATGTTAATAACATGACATCTACCAGGTCACTCCTGTCTACCGCCT
CGGCTCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAACGGCCCTGTCCAAGCCCTCA
TGGAGGTGCATGAGGACTTCTTCTATAACAGGGAGGCATCTACAGCCACAGCCAGTGAGC
CTTGGGAGGCCAGAGAGATAACGCCGGCATGGGACCCACTCAGTCAAGATCACAGGATGGGG
AGAGGAGACGCTGCCAGATGGAAGGAGCTCAAATACTGACTGCCAACCTCTGGGCC
CAGCCTGGGCGAGAGGGCCACTTCCGCATCGTGCCTGGCTCAATGAGTGCACATCGAG
AGCTTGTGCTGGCGCTGGGCCGCTGGGATCCAGGCTAACGGCCGGGAAGAGGCCCAATG
GGCGGTGACCCAGCCTCGCCGACAGAGGCCGGCGCAGGCCGGCAGGGCGCTAAT
CCCGCGCGGGTCTCGTACGCAGGCCCGCCTGGGAGGCCGGCAGGGAGACTGGCG
GAGCCCCAGACCTCCAGTGGGACGGGGCAGGGCCTGGGAAGAGCACAGCTGCAG
ATCCCAGGCCTCTGGGCCCAACTCAAGACTACCAAAAGCCAGGACACCTCAAGTCTCCAGC
CCCAATACCCACCCAACTCCGTATTCTTTTTTTAGACAGGGTCTGCTCCG
TTGCCAGGTTGGAGTGCAGTGGCCATCAGGGCTCACTGTAACCTCCGACTCCTGGTTCA
AGTACCCCTCCCACCTCAGCCTCTCAAGTAGCTGGACTACAGGTGCACCAACACCTGGC
TAATTTTGATTTTGAAAGAGGGGGTCTCACTGTGTTGCCAGGCTGGTTCAACT
CCTGGCTCAAGCGGCCACCTGCCTCCGCTCCAAAGTGCAGGGATTGCAGGCATGAGCC
ACTGCACCCAGCCCTGTATTCTATTCTCAGATATTATTTCTTCACTGTTAAAAA
TAAAACCAAAGTATTGATAAAAAAAAAAA

FIGURE 6

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223
><subunit 1 of 1, 164 aa, 1 stop
><MW: 18359, pI: 7.45, NX(S/T): 1
MWRCPLGLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAAGGRYEQDLCCRGRADDC
ALPYLGAICYCDLFCNRTVSDCCPDFWDFCLGVPPPFPPPIQGCMHGGRIYPVLGTYWDNCNR
CTCQENRQWHGGSRHDQSHQPGQLWLAGWEQRLLGHDPG
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N-glycosylation site.

amino acids 78-82, 161-165

Casein kinase II phosphorylation site.

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,
411-415

N-myristoylation site.

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,
269-275, 378-384, 442-448

Amidation site.

amino acids 26-30, 318-322

Eukaryotic thiol (cysteine) proteases histidine active site.

amino acids 398-409

FIGURE 7

AGGCTCCTTGGCCCTTTCCACAGCAAGCTTNTGCNATCCGATTGTTGTCTCAAATCCA
ATTCTCTTGGGACACATNACGCCGTCTTNGCCCCAGAACCTGCTGTCTGTACACCCAC
CAGCAGCAGGGCTGCCCGNTGGCGTCTCGATGGTGCCTGGTGGTCCTGCGTCGCCGAGG
GNTGGTGTCTGACCACTGCTACCCCTCTCGGGCCGTGAACGAGACGAGGCTGGCCCTGCGC
CCCCCTGTATGATGCACAGCCGAGCCATGGTCGGGCAAGGCCAGGCCACTGCCACTGC
CCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCTCGGCTC
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTATGGAGG
TGCATGAGGACTTCTTCCCTATAACAAGGGAGGCATCTACAGCCACACGCCAGTGAGCCTGGG
AGGCCAGAGAGATACCGCCGGCATGGGACCCACTCAG

FIGURE 8

GCTGCTTGCCTGTTGATGGCAGGCTTGCCTGCAGCCAGGCAGTCCTGCTGTGCTACT
CCTGCAAAGCCCAGGTGAGCAACGAGGACTGCCTGCAGGTGGAGAACTGCACCCAGCTGGGG
GAGCAGTGCTGGACC CGCGCATCCGCAGTTGGCCTCCTGACCGTCATCAGCAAAGGCTG
CAGCTTGAACTGCGTGGATGACTCACAGGACTACTACGTGGCAAGAAGAACATCACGTGCT
GTGACACCGACTTGTGCAACGCCAGCGGGGCCATGCCCTGCAGCCGGCTGCCGCATCCTT
GCGCTGCTCCCTGCACTCGGCCTGCTGCTCTGGGGACCCGGCCAGCTATAGGCTCTGGGGGG
CCCCGCTGCAGCCCACACTGGGTGTGGTCCCCAGGCCTCTGTGCCACTCCTCACAGACCTG
GCCCACTGGGAGCCTGTCCTGGTTCTGAGGCACATCCTAACGCAAGTCTGACCATGTATGT
CTGCACCCCTGTCCCCCACCCCTGACCCCTCCATGGCCCTCTCCAGGACTCCCACCCGGCAGA
TCAGCTCTAGTGACACAGATCCGCCTGCAGATGGCCCTCCAACCCTCTTGCTGCTGTTTC
CATGGCCCAGCATTCTCCACCCCTAACCCCTGTGCTCAGGCACCTCTCCCCCAGGAAGCCTT
CCCTGCCAACCCATCTATGACTTGAGCCAGGTCTGGTCCGTGGTCCCCCGCACCCAGCA
GGGGACAGGCACTCAGGAGGGCCCAGTAAAGGCTGAGATGAAGTGGACTGAGTAGAAACTGGA
GGACAAGAGTCGACGTGAGTTCTGGAGTCTCCAGAGATGGGGCCTGGAGGCCTGGAGGAA
GGGGCCAGGCCTCACATTGCTGGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTT
AATAAACACCTGTTGGATAAGCCAAAAAAA

FIGURE 9

MTHRTTWARRTSRAVTPTCATPAGPMPCSRLPPSLRCSLHSACCSGDPASYRLWGAPLQPT
LGVVPQASVPLLTDLAQWEPVLVPEAHPNASLTMYVCTPVPHDPPMALSRTPTRQISSLDT
DPPADGPSNPLCCCFHGPAGFSTLNPVLRHLFPQEAFPAHPIYDLSQVWSVVSPAPSRGQALRRAQ

Signal peptide:

amino acids 1-47

N-glycosylation site.

amino acids 31-35, 74-78, 84-88

Casein kinase II phosphorylation site.

amino acids 22-26, 76-80

N-myristoylation site.

amino acids 56-60

Amidation site.

amino acids 70-74

FIGURE 10

CCACCGCGTCCGAAACCTCTCCAGCGATGGGAGCCGCCGCCTGCTGCCAACCTCACTCTGT
GCTTACAGCTGCTGATTCTCTGCTGTCAAACACTCAGTGAGGGACCAGGGGCCATGACC
GACCAGCTGAGCAGGCGGCAGATCCCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA
CGTGCAGGTACCGGGCGTCGCATCTCCGCCACCGCCGAGGAACAGCAAAAGTTGCCAAGC
TCATAGTGGAGACGGACACGTTGGCAGCCGGTTCGCATCAAAGGGCTGAGAGTGAGAAG
TACATCTGTATGAACAAGAGGGCAAGCTCATCGGAAGCCCAGCGGAAGAGCAAAGACTG
CGTGGTCACGGAGATCGTGCTGGAGAACAACTATAACGCCCTCCAGAACGCCGGCACGAGG
GCTGGTTCATGGCCTTCACGCCAGGGCGGCCAGGCTCCGCAGCCGCCAGAAC
CAGCGCAGGCCCACTCATCAAGCGCCTCTACCAAGGCCAGCTGCCCTCCCCAACACGC
CGAGAACAGAACAGCAGTTCGAGTTGTGGCTCGCCCCACCCGCCGGACCAAGCGCACAC
GGCGGCCCAAGCCCCTCACGTAGTCTGGGAGGCAGGGGCAGCAGCCCCTGGCCGCCCTCCC
CACCCCTTCCCTTTAATCCAAGGACTGGCTGGGTGGCGGGAGGGAGCCAGATCCCC
GAGGGAGGACCCCTGAGGGCCGCAAGCATCCGAGCCCCCAGCTGGGAAGGGCAGGCCGGTG
CCCCAGGGCGGCTGGCACAGTGCCCCCTCCCGACGGTGGCAGGCCCTGGAGAGGAAC
GAGTGTACCCCTGATCTCAGGCCACCAGCCTCTGCCGCCCTCCAGCCGGCTCTGAAGCC
CGCTGAAAGGTCAAGCAGTGAAGGCCTTGAGACAAACCGTCTGGAGGTGGCTGTCTCAAAA
TCTGCTTCTCGGATCTCCCTCAGTCTGCCCTCAGGCCCCAAACTCCTCCTGGCTAGACTGTA
GGAAGGGACTTTGTTGTTGTTGTTCAAGAAAAAGAAAGGGAGAGAGAGGAAATAG
AGGGTTGTCCACTCCTCACATTCCACGACCCAGGCCTGCACCCCCACCCCAACTCCCAGCCC
CGGAATAAAACCATTTCCCTGC

FIGURE 11

MGAARLLPNLTLCLQQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRI
SATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNKRGKLIGKPSGKSKDCVFTEIVLE
NNYTAFQNARHEGWFMAFTRQGRPRQASRSRQNQREAHFIKRLYQGQLPFPNHAEKQKQFEF
VGSAPTRRTKRTRRPQPLT

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 9-13, 126-130

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 60-64

Casein kinase II phosphorylation site.

amino acids 65-69

Tyrosine kinase phosphorylation site.

amino acids 39-48, 89-97

N-myristoylation site.

amino acids 69-75, 188-194

Amidation site.

amino acids 58-62

HBGF/FGF family signature.

amino acids 103-128

FIGURE 12

ACTTGCCATCACCTGTTGCCAGTGTGGAAAATTCTCCCTGTTGAATTTTTGCACATGGAG
GACAGCAGCAAAGAGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTAC
CATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTTCTGGACTTCACAGAACCCCATCCAGT
CATTGATTGCTGTTATTTTTCTTTTCTTCCCACACATTGTATTTAT
TTCCGTACTTCAGAAATGGGCTACAGACCAAAAGTGGCCAGCCATGGGCTTTTCCCT
GAAGTCTTGGCTTATCATTCCTGGGCTACTCACAGGTGTCAAACCTCTGGCCTGCC
CTAGTGTGTGCCGCTGCAGAGGAACCTTGCTACTGTAATGAGCGAAGCTGACCTCAGTG
CCTCTGGGATCCGGAGGGCGTAACCGTACTCTACCTCCACAACAACCAAAATTAAATGC
TGGATTTCCCTGCAGAACTGCACAATGTACAGTCGGTGACACGGCTACCTGTATGCCAAC
AACTGGACGAATTCCCCATGAACCTCCAAGAATGTCAGAGTTCTCCATTGCAAGGAAAAC
AATATTAGACCATTTCACGGGCTGCTTGCCTGAAGCTGAAGAGCTGCACCT
GGATGACAACCTCCATATCCACAGTGGGGTGGAAAGACGGGCCCTCCGGGAGGCTATTAGCC
TCAAATTGTTGTTTGTCTAAGAATCACCTGAGCAGTGTGCCCTGTTGGCTTCCCTGGA
TTGCAAGAGCTGAGAGTGGATGAAAATCGAATTGCTGTATATCCGACATGCCCTCCAGAA
TCTCACGAGCTGGAGCGTCTTATTGGACGGAACCTCTGACCAACAAGGGTATGCCG
AGGGCACCTCAGCCATCTCACCAAGCTCAAGGAATTTCATTGTAACGTAATTGCTGTCC
CACCCCTCCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTGCAAGGACAACCA
AAACACATTCCATTGACAGCCTCTCAAATCTCGTAAGCTGGAACGGCTGGATATATCCA
ACAACCAACTGCGGATGCTGACTCAAGGGGTTTGATAATCTCTCAACCTGAAGCAGCTC
ACTGCTCGGAATAACCCCTGGTTTGTGACTGCAGTATTAAATGGGTACAGAAATGGCTCAA
ATATATCCCTTCATCTCAACGTGCGGGGTTCATGTGCCAAGGTCTGAACAAGTCCGGG
GGATGGCGTCAGGGAAATTAAATATGAATCTTGTCCCTGCCCACACGACCCCGGCCCTG
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TCCAAACCTAGCAGAAGCTACACGCCCTCAAACCTACCGAAACTTCCCACGATT
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CAAACTCACATGGGTAAAATGGGCCACAGTTAGTAGGGGGCATGTTCAAGGAGCGCATAG
TCAGCGGTGAGAAGCAACACCTGAGCCTGGTAACCTAGAGCCCCGATCCACCTATGGATT
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AGGACAACCTCCATCCTGGAGATGACAGAAACCAGTTTCAGATCGTCTCTTAAATAACGAT
CAACTCCTAAAGGAGATTTCAGACTGCAGCCATTACACCCAAATGGGGCATTAATTA
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CACACTCGTGTGTCACATAAGACACGCAGATTACATTGATAAAATGTTACACAGATGCAT
TTGTGCATTGAAATACTCTGTAATTATACGGGTACTATATAATGGGATTAAAAAAAGTG
CTATCTTCTATTCAAGTTAATTACAAACAGTTGTAACTCTTGCTTTAAATCTT

FIGURE 13

MGLQTTKWP SHG AFFL KSWL IIS LGL YSQ VSK LLA CPS VCR CDR N FV YCN ERS LT SVP LGIP
EGTV VL YLHN NQIN NAGF PAEL HNV QSV HTV YLYGNQLDEFPMNLPKNVRVLH LQENNIQTI
SRA ALAQLLKLEELHLDDNSISTVGVEDGAFREAI SLKLLFLSKNHLSSVPVGLPVDLQELR
VDEN RIAVI SDMAF QNL TS LERLIV DGN LLTNKGIAEGTFSHTKLKEFSIVRN SLSH PPPD
LPGTHLIRLYLQDNQINHIPLTA FSNL RKL ERLDI SNNQLRMLTQGVFDNLSNLKQLTARN
PWFCD CSIKWVTEWLKYIPSSLNVRGFM CQGPEQVRGM AVERELNMNLLSCPTTPGLPLFTP
APSTASPTTQPPTTLSIPNPSRSYTPPTPTTSKLPTIPDWDG RERVT PPI SERIQLSIHFVND
TSIQVSWLSLEFTVMAYKLTWVKM GHSLVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPL
DAFN YRAVED TICSEATTHASYLNNGSNTASSHEQTTSHSMGSPFLLAGLIGGAVIFV LVVL
LSVFCWHMHKKGRYTSQWKYNRGRRKDDYCEAGTKKD NSILEMTETSFQIVSLNNDQLLKG
DFRLQPIYTPNGGINYTDCHI PNNMRYCNS SVPD LEHCHT

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 542-561

N-glycosylation site.

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

Casein kinase II phosphorylation site.

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

Tyrosine kinase phosphorylation site.

amino acids 319-328

N-myristoylation site.

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,
522-528, 545-551, 633-639

Amidation site.

amino acids 581-585

Leucine zipper pattern.

amino acids 164-186

Phospholipase A2 aspartic acid active site.

amino acids 39-50

FIGURE 14

ACTTGGAGCAAGCGGCGGCCGGAGACAGAGGCAGAGGCAGAAGCTGGGCTCCGTCCGCCTCCCACGAGCG
ATCCCCGAGGAGAGCCGCGCCCTCGCGAGGCCAAGAGGCCACGAGGAAGACCCGGTGGCTGCGCCCTGCC
TCGCTTCCCAGGCAGGCCGGCTGCAGCCTGCCCTCTGCTCGCCTGAAAATGGAAAAGATGCTCGCAGGCT
GCTTTCTGCTGATCCTCGAACAGATCGCCTCCCTGCCAGGGAGCGGTACGTGGAGGTCCATCT
CTAGGGGCAGACACGCTCGAACCCACCCGCAGACGCCCTCTGGAGAGTTCCTGTGAGAACAGCAGGCCAGACC
TGGTTTCATCATTGACAGCTCGCAGTGTCAACACCCATGACTATGCAAAGGTCAAGGAGTTCATGTGGACA
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AGTTCTCCCTCAAGACCTCAAGAGGAAGTCCGAGGTGGAGCGTGTCAAGAGGATGCGGCATCTGTCACGG
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AGGCACGGGACACGGGCATCTTAATCTTGCCATTGGTGTGGGCCAGGTAGACTTCAACACCTTGAAAGTCCATTG
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GCTCATACGTCTGCAGGTGCAAACAAGGCTACATTCTCAACTCGGATCAGACGACTTGCAGAACATCCAGGATCTGT
GTGCCATGGAGGACCAACTGTGAGCAGCTCTGTGTGAATGTGCCGGCTCCTCGTCTGCCAGTGCTACAGTG
GCTACGCCCTGGCTGAGGTGGGAAGAGGTGTGGACTACTGTGCCCTAGAAAACACGGATGTGAAC
ATGAGTGTGAAATGCTGATGGCTCCTACCTTGCCACTGAGGATTGTCTTAACCCAGATGAAAAAA
CGTGCACAAGGATCAACTACTGTGCACGAAACAACCCCTGTGAGGATGAGTGTGTCACATGGAGGAGAGCT
ACTACTGCCGCTGCCACCGTGGCTACACTCTGGACCCCAATGGCAAACACCTGCAGCCAGTGGACACTGTGCAC
AGCAGGACCATGGCTGTGAGCAGCTGTGTAACACGGAGGATTCTCGTCTGCCAGTGCTCAGAAGGCTTCC
TCATCAACGAGGACCTCAAGACCTGCTCCCGGGTGGATTACTGCCCTGCTGAGTGAACATGGGTGTGAATACTCCT
GTGTCAACATGGACAGATCCTTGCTGTCACTGTGCTCTGAGGGACACGTGCTCCCGAGCGATGGAAAGACGTGTG
CAAAATTGGACTCTTGTGCTCTGGGGACACCAGGTTGTGAACATTGTGTAAGCAGTGAAAGATTGTTGTG
GCCAGTGCTTGAAAGGTTATATACTCCGTGAAGATGGAAAAACCTGCAAGAGAAAGATGTCGCCAAGCTATAG
ACCATGGCTGTGAACACATTTGTGTAACAGTGACGACTCATACACGTGCGAGTGCTGGAGGGATTCCGGCTCG
CTGAGGATGGGAAACGCTGCCGAAGGAAGGATGTGCAATCAACCCACATGGCTGCGAACACATTGTGTTA
ATAATGGGAACTCCTACATGCTCAAATGCTCAGAGGATTGTGTTCTAGCTGAGGACGGAAGACGGTGCAAGAAAT
GCACTGAAGGCCAATTGACCTGGTCTTGATGATGGATCCAAGAGTCTTGAGAAGAGAATTGGAGGTG
TGAAGCAGTTGTCACTGGAATTATAGATTCCCTGACAATTCCCCAAAGCCGCTCGAGTGGGCTGCTCCAGT
ATTCCACACAGGTCCACACAGAGTTCACTCTGAGAAACTCAACTCAGCCAAAGACATGAAAAAGCCGTGGCC
ACATGAAATACATGGGAAAGGGCTTATGACTGGCTGCCCTGAAACACATGTTGAGAGAAGTTTACCCAAAG
GAGAAGGGCCAGGCCCTTCCACAAGGGTGCAGAGCAGCCATTGTGTTCAACGGACGGACGGCTCAGGATG
ACGTCCTCGAGTGGGCCAGTAAAGCCAAGGCCAATGGTATCACTATGTTGCTGTTGAGGAAAGCCATTG
AGGAGGAACATACAAGAGATTGCCCTGAGGCCACAAACAAGCATCTTCTATGCCGAAGACTCAGCACAAATGG
ATGAGATAAGTGGAAAAACTCAAGAAAGGATCTGTGAAGCTCTAGAAAGACTCCGATGGAAGACAGGACTCTCCAG
CAGGGGAACATGCCAAAAGGTCCAACAGCCAACAGAAATCTGAGCCAGTCACCAAAATATCCAAGACCTACTTT
CCTGTTCTAATTGTGCAACACAGATATCTGTTGAAGAAGACAATCTTACGGCTCACACAAAGCTTT
CCCATTCAACAAACCTCAGGAAGGCCCTTGGAGAAAACACGATCAATGCAATGTGAAAACCTTATAATGT
TCCAGAACCTGCAAACGAAGAAGTAAGAAAATAACACAGCGTTAGAAGAAATGACACAGAGAATGGAAGGCC
TGGAAAATGCCCTGAGATACAGATGAAGATTAGAATCGGCACACATTGTTAGTCATTGTATCACGGATTACAAT
GAACCGAGTGCAGAGGCCAAAGCTCAGGCTATTGTTAAATCAATAATGTTGTGAAGTAAACAAATCAGTACTGA
GAAACCTGGTTGCCACAGAACAAAGACAAGAAGTATAACACTAATCTGTTATAAATTATCTAGGAAAAAAACCT
TCAGAACATTCTAAGATGAATTACCAAGGTGAGAATGAATAAGCTATGCAAGGTATTGTAAATATACTGTGGACAC
AACTGCTCTGCCATCCTGCCATTGTGCAATCTCATTGACTATACGATAAAAGTTGCACAGTCTTACT
CTGTAGAACACTGCCATAGGAAATGCTGTTTTGTACTGGACTTACCTTGATATATGTATATGGATGTATG
CATAAAATCATAGGACATATGTACTTGTGAAACAAGTGGATTAAATACAATATTAAAATTCCACTTCAG

FIGURE 15

MEKMLAGCFLILGQIVLLPAEARERSRGRSISRGHRARTHPTALLESSCENKRADLVFII
DSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTFRKSEVERAV
KMRHLSTGTMGLAIQYALNIAFSEAEGARPLRENVPRVIMIVTDGRPQDSVAEVAAKARD
TGILIFAIVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFQKKLCTAHMCSTLEHN
CAHFCINIPGSYVCRKQGYILNSDQTTCRIQDLCAMEDHNCEQLCVNPQGSFVCQCYSGYA
LAEDGKRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCTRINYCALNKPGC
EHECVNMEESYYCRCHRGYTLDPNGKTCRVDHCAQQDHGCEQLCLNTEDSFVCQCSEGFLI
NEDLKTCSRVDYCLLSDHGCEYSCVNMDRSFACQCPEGHVLRSDBGKTCAKLDSALGDHGCE
HSCVSSEDSFVCQCPEGYILREDGKTCRRKDVCQAIDHGCEHICVNSDDSYTCECLEGFR
LAEDGKRCRKDVCKSTHHGCEHI CVNNNGNSYICKCSEGFLAEDGRRCKKCTEGPIDLVFVID
GSKSLGEENFEVVVKQFVTGIIDS LTISPKAARVGLLQYSTQVHTEFTLRNFNSAKDMKKAVA
HMKYMGKGSMTGLALKHMFRSFTQGEGARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKAN
GITMYAVGVGKAIEELQEIASEPTNKHLFYAEDFSTMDEISEKLKGICEALEDSDGRQDS
PAGELPKTVQQPTESEPVTINIQDLLSCSNFAVQHRYLFEEDNLLRSTQKLHSHTKPSGSPL
EEKHDQCKCENLIMFQNLANEEVRKLTQRLEEMTQRMEALENRLRYR

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 221-225

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 115-119, 606-610, 892-896

Casein kinase II phosphorylation site.

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247,
401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784,
781-785, 819-823, 866-870

N-myristoylation site.

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500,
639-645, 690-696, 752-758, 792-798

Amidation site.

amino acids 314-318, 560-564, 601-605

Aspartic acid and asparagine hydroxylation site.

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464,
540-546, 581-587

FIGURE 16

GGAGCCGCCCTGGGTGTCAGCGCTCGGCTCCCGCGCACGCTCCGGCCGCGCAGCCTCG
GCACCTGCAGGTCCGTGCGTCCCGCGCTGGCGCCCTGACTCCGTCCCGGCCAGGGAGGGC
CATGATTCCTCCCTCCGGGCCCTGGTGACCAACTTGCTGCGGTTTTGTTCTGGGCTGA
GTGCCCTCGCGCCCCCTCGCGGCCAGCTGCAACTGCAC TTGCCGCCAACCGGTTGCAG
GCGGTGGAGGGAGGGAAAGTGGTGCTTCCAGCGTGGTACACCTTGCACGGGAGGTGTCTC
ATCCCAGCCATGGGAGGTGCCCTTGTGATGTGGTTCTCAAACAGAAAGAAAAGGAGGATC
AGGTGTTGTCTACATCAATGGGTACAACAAGCAAACCTGGAGTATCCTGGTCTACTCC
ATGCCCTCCCGAACCTGTCCCTGCGGCTGGAGGGCTCCAGGAGAAAGACTCTGGCCCTA
CAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCCACAGCATAAAACCT
TAGAACTCAATGTACTGGTTCTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCAT
GTGGGGCAAACGTGACCTGAGCTGCCAGTCTCCAAGGAGTAAGCCGCTGTCCAATACCA
GTGGGATCGGCAGCTCCATCCTCCAGACTTCTTGACCAGCATTAGATGTCATCCGTG
GGTCTTTAACGCTCACCAACCTTCGTCTTCCATGGCTGGAGTCTATGTCAGGCCAC
AATGAGGTGGGCACTGCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCTGGAGCTGC
AGTGGTTGCTGGAGCTGTTGGTACCTGGTGGACTGGGTTGCTGGCTGGCTGGTCC
TCTGTACCACCGCCGGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCC
ATTGCTCCCGAACCTGCCCTGGCCAAGAGCTCAGACACAATCTCCAAGAATGGGACCC
TTCCTCTGTACCTCCGACGAGCCCTCCGCCACCCATGGCCCTCCAGGCCTGGTGCAT
TGACCCCCACGCCAGTCTCCAGCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGAT
GGGGCCACCCCAACCAATATCCCCATCCCTGGTGGGTTCTCCTCTGGCTTGAGCCG
CATGGGTGCTGTGCCTGTGATGGTGCCCTGCCAGAGTCAAGCTGGCTCTGGTATTGATGAC
CCCACCACTCATTGGCTAAAGGATTGGGTCTCTCCTTCTATAAGGGTACACCTCTAGCAC
AGAGGCCTGAGTCATGGAAAGAGTCACACTCCTGACCCCTAGTACTCTGCCACCTCTC
TTTACTGTGGAAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA
AGTGGATCTGGAATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCTTATGAAGCCAGCTG
CTGAAATTAGCTACTCACCAAGAGTGAGGGCAGAGACTCCAGTCAGTCAAGTCTCCAGGC
CCCCTTGATCTGTACCCACCCCTATCTAACACCACCCCTGGCTCCACTCCAGCTCCCTGT
ATTGATATAACCTGTCAAGGCTGGCTGGTTAGGTTTACTGGGCAGAGGATAGGAAATCTC
TTATTAAAACATGAAATATGTGTTGTTTCAATTGCAAATTAAATAAGATAACATAA
TGTGGTATGAAAAA

FIGURE 17

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHL PANRLQAVEGGEVVLPAWYTLHGEVSS
SQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKDGPY
SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSQSPRSKPQAVYQ
WDRQLPSFQTFFAPALDVIRGSSLTNLSSSMAGVYVCKAHNEVGTACNCNTLEVSTGPGAA
VVAGAVVGTIVGLGLLAGLVLLYHRRGKALEEPANDIKAEDAIAPRTLWPWPKSSDTISKNGTL
SSVTSARALRPPHGPPRGALTPTPSLSSQALPSPRLPTTDGAHPQPISPIPGVSSSGLSR
MGAVPVMVPAQSQAGSLV

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 245-267

N-glycosylation site.

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

N-myristoylation site.

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,
262-268, 308-314, 363-369, 364-370

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 164-175

FIGURE 18

CGCCACCACTGGGCCACCGCCAATGAAACGCCTCCGCTCCTAGTGGTTTTCCACTTG
TTGAATTGTTCTATACTCAAATTGACCAAGACACCTGTCTCCAAATGAAAATGTGA
AATAACGCAATGGAATTGAAGCCTGCTATTGCAACATGGGATTTCAGGAAATGGTGTACAA
TTTGTGAAGATGATAATGAATGTGGAAATTAACTCAGTCCTGTGGCGAAAATGCTAATTGC
ACTAACACAGAAGGAAGTTATTATTGTATGTGTACCTGGCTTCAGATCCAGCAGTAACCA
AGACAGGTTATCACTAATGATGGAACCGTCTGTATAGAAAATGTGAATGCAAACGTGCCATT
TAGATAATGTCTGTATAGCTGAAATATTAAATAAAAACCTTAACAAAAATCAGATCCATAAAA
GAACCTGTGGCTTGTACAAGAAGTCTATAGAAATTCTGTGACAGATCTTCACCAACAGA
TATAATTACATATAGAAATTAGCTGAATCATCTTCACTAGTTACAAGAACAAACA
CTATCTCAGCCAAGGACACCCTTCTAACTCAACTCTTACTGAATTGTAACAGAACCGTGAAT
AATTGGTCAAAGGGATACATTGTAGTTGGACAAGTTATCTGTGAATCATAGGAGAAC
ACATCTTACAAAATCATGCACACTGTTGAACAAGCTACTTAAAGGATATCCCAGAGCTTCC
AAAAGACCACAGAGTTGATACAAATTCAACGGATATAGCTCTCAAAGTTTCTTTTGAT
TCATATAACATGAAACATATTCTCATCTCATATGAATATGGATGGAGACTACATAAATATATT
TCCAAAGAGAAAAGCTGCATATGATTCAAATGGAATGTTGAGCTTCAGTCTCAATGAGCTCAAACCC
AATTCTGAAGAGGAGGAAAGAGTCATATCTTCAGTAATTCACTGAGCTCAATGAGCTCAAACCC
ACCCACATTATATGAACATTGAAAAAAATAACATTACATTAAGTCATCGAAAGGTACAGATA
GGTATAGGAGTCTATGTGCATTGGAAATTACTCACCTGATACCATGAATGGCAGCTGGTCT
TCAGAGGGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCT
GACACATTTGCAATTGATGTCCTCTGGCCTTCCATTGGTATTAAGATTATAATATT
TTACAAGGATCACTCAACTAGGAATAATTATTCAGTGAATTGCTTCTGGCCATATGCATT
ACCTTCTGGTCTTCAGTGAATTCAAAGCACCAGGACAACAATTCAAACAAATTCTTGCTG
TAGCCTATTCTTGCTGAATTGTTCTTCTGGATCAATACAAACTAAAGCTCT
TCTGTTCAATCATTGCCGGACTGCTACACTACTTCTTTAGCTGCTTGCATGGATGTGC
ATTGAAGGCATACATCTATCTCATTGTTGTGGGTGTCATCTACAACAAGGGATTGGCA
CAAGAATTTTATATCTTGGCTATCTAACGCCAGCCGTGGTAGTTGGATTTCGGCAGCAC
TAGGATACAGATATTATGGCACACCAAAGTATGTTGGCTTAGCACCAGAAACACTTTATT
TGGAGTTTATAGGACCAGCATGCCATTCTGTTAATCTCTGGCTTTGGAGTCAT
CATATAACAAAGTTTCTGCACACTGCAGGGTTGAAACCAAGTTAGTTGCTTGGAGAAC
TAAGGTCTTGCAAGAGGAGGCCCTCGCTCTCTGTTCTCTGGCACCACCTGGATCTT
GGGTTCTCATGTTGTGCACGCATCAGTGGTACAGCTTACACTCTCACAGTCAGCAATGC
TTTCCAGGGATGTCATTGTTATTCTGTGTTTATCTAGAAAGATTCAAGAAGAAT
ATTACAGATTGTCAAAATGCCCCGTGTTGGATGTTAAGGTAAACATAGAGAAC
GTGGATAATTACAACACTGCACAAAATAAAAATTCCAAGCTGTGGATGACCAATGTATAAAA
TGACTCATCAAATTATCCAATTATTAACACTAGACAAAAGTATTAAATCAGTT
GTTTATGCTATAGGAACACTGTAGATAATAAGGAAAATTATGTATCATATAGATATACTATGT
TTTCTATGTGAAATAGTCTGTCAAAATAGTATTGCAAGATATTGGAAAGTAATTGGTT
CTCAGGAGTGTATCACTGCACCCAAGGAAAGATTCTTCTAACACGAGAAGTATATGAA
TGTCTGAAGGAAACCACTGGCTGATATTCTGTGACTCGTGTGCCTTGAAACTAGTCC
CCTACCACCTCGGTAAATGAGCTCATTACAGAAAGTGGAACATAAGAGAACAGGGCAGA
ATATCAAACAGTGAAGGAAATGATAAGATGTATTGAAATGAACACTGTTTCTGTAGAC
TAGCTGAGAAATTGTTGACATAAAATAAGAATTGAAGAAACACATTACCAATTGAA
TTGTTCTGAACCTAAATGTCCACTAAACAACTTAGACTCTGTTGCTAAATCTGTTCTT
TTCTAATATTCTAAAAAAAAAGGTTACCTCCACAAATTGAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAA

FIGURE 19

MKRLPLVVVFSTLLNCSYTQNCTKTPCLPNAKCEIRNGIEACYCNMGSGNGVTICEEDDNEC
GNLTQSCGENANCTNTESYYCMCVPGFRSSSNQDRFITNDGTVCIENVANCHLDNV CIAA
NINKTLTKIRSIKEPVALLQEYVNRNSVTDLSPTDIITYIEILAESSLLGYKNNTISAKDTL
SNSTLTERFVKT VNNFVQRDTFVWWDKLSVNHRRTHLTKLMHTVEQATLRISQSFQKTTEFDT
NSTDIALKVFFFDSYNMKHIHPHMNMDGYINIFPKRKAAYDSNGNVAVAFLYYKSIGPLLS
SSDNFLLKPQNYDNSEEERVISSVISVSMSSNPPTLYELEKITFTLSHRKVDYRSLCAF
WNYSPDTMNGWSSEGCELTYSNETHTSCRNCNLTHFAILMSSGPSIGIKDYNILTTRITQLG
IIISLICLAICIFTFWFFSEIQSTRTTIHKNLCCSLFLAEVFLVGINTNTNKLFCIIAGL
LHYFFLAFAFWMCIEGIHLYLIVVGVIYNKGFLHKNFYIFGYLSPAVVVGFSAA LGYRYYGT
TKVCWLSTENNFIFS FIGPACLIILVNLLAFGVIIYKVFRHTAGLKPEVSCFENIRSCARGA
LALLFLLGTTWIFGVLVVHASVVTAYLFTVSNAFQGMFIFLFLCVLSRKI QEEYYRLFKNV
PCCFGCLR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,
648-664

N-glycosylation site.

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,
188-192, 249-253, 381-385, 395-399

Glycosaminoglycan attachment site.

amino acids 49-53

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 360-364

Casein kinase II phosphorylation site.

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,
346-350, 608-612

Tyrosine kinase phosphorylation site.

amino acids 36-44, 669-677, 670-678

N-myristoylation site.

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,
434-440, 480-486, 521-527

Aspartic acid and asparagine hydroxylation site.

amino acids 75-87

FIGURE 20

TGGAAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAATATTTCCAAAGNG
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTGATTTTATATTATAAGAGTAT
TGGTCCTTGTTCATCATCTGACAACCTTATTGAAACCTCAAAATTATGATAATTCT
GAAGAGGAGGAAAGAGTCATATCTCAGTAATTCAGTCTCAATGAGCTCAAACCCACCCAC
ATTATATGAACCTGAAAAAAATAACATTTACATTAAGTCATCGAAAGGTACAGATAGGTATA
GGAGTCTATGTGGCATTGGAAACTCACCTGATACCATGAATGGCAGCTGGTCTCAGAG
GGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA
TTTGCAATTGATGTCCTCTGGCCTTCCATTGGTATTAAAGATTATAATATTCTTACAA
GGATCACTCAACTAGGAATAATTATTCACTGATTGTCTGCCATATGCATTTTACCTTC
TGGTTCTTCAGTGAAATTCAAAGCACCAGGA

FIGURE 21

GCTCCCAGCCAAGAACCTCGGGGCCGCTGCGCGGTGGGGAGGGAGTTCCCCGAAACCCGGCCG
CTAAGCGAGGCCTCCTCCCTCCCGCAGATCCGAACGGCCTGGCGGGGTCAACCCGGCTGGGA
CAAGAAGCCGCCGCCTGCCTGCCCGGGCCGGAGGGGCTGGGCTGGGCCGGAGGCAGG
GGTGTGAGTGGGTGTGTGCGGGGGCGGAGGCTTGATGCAATCCCGATAAGAAATGCTCGGG
TGTCTGGCACCTACCGTGGGCCGTAAGGCCTACTATATAAGGCTGCCGGCCGGAG
CCGCCGCGCCGTCAAGACAGGAGCGCTCGCTCAGGATCTAGGGCACGACCATCCCAACCC
GGCACTCACAGCCCCCGCAGCGCATCCCGTCGCCGCCAGCCTCCCGCACCCCCATGCCGG
AGCTGCGCCAGAGAGCCCCAGGGAGGTGCCATGCGGAGCGGGTGTGGTGGTCCACGTATGG
ATCCTGGCGGCCTCTGGCTGGCGTGGCCGGCGCCCCCTGCCTCTCGACGCGGGCC
CCACGTGCACTACGGCTGGGCGACCCCATCCGCCTGCACCTGTACACCTCCGGCCCC
ACGGGCTCTCAGCTGCTTCCTGCGCATCCGTGCCGACGGCGTGGACTGCGCGGGGC
CAGAGCGCGCACAGTTGCTGGAGATCAAGGCAGTCGCTTGCGGACCGTGGCATCAAGGG
CGTGACAGCGTGCCTGACCTCTGCATGGCGCCGACGGCAAGATGCAGGGCTGCTCAGT
ACTCGGAGGAAGACTGTGCTTCGAGGAGGAGATCCGCCAGATGGCTACAATGTGTACCGA
TCCGAGAAGCACCGCTCCGGCTCCCTGAGCAGTGCCTACAGGGCAGCTGTACAAGAA
CAGAGGCTTCTTCCACTCTCATTCTGCCTGCCCAGTGCCTGCCATGGTCCCAGAGGAGCCTG
AGGACCTCAGGGGCCACTTGAATCTGACATGTTCTTCGCCCCCTGGAGACCGACAGCATG
GACCCATTGGGCTTGTCAACGGACTGGAGGCCGTGAGGAGTCCAGCTTGAGAAGTAAC
GAGACCATGCCCGGCCCTTCACTGCTGCCAGGGCTGTGGTACCTGCAGCGTGGGGACG
TGCTTCTACAAGAACAGTCTGAGTCCACGTTCTGTTAGCTTAGGAAGAACATCTAGAA
GTTGTACATATTCAAGAGTTCCATTGGCAGTGCCTAGCTAGCAATAGACTTGTCTGAT
CATACATTGTAAGCCTGTAGCTGCCAGCTGCTGCCCTGGCCCCATTCTGCTCCCTCGA
GGTTGCTGGACAAGCTGCTGCACTGTCTCAGTTCTGCTGAATACCTCCATCGATGGGAAC
TCACTTCTTGAAAAATTCTTATGTCAAGCTGAAATTCTCTAAATTCTCATCACTTC
CCCAGGAGCAGCCAGAACAGACAGGCAGTAGTTAATTCAAGAACAGGTGATCCACTCTGTA
AAACAGCAGGTAATTCACTCAACCCATGTGGAATTGATCTATCTACTTCCAGGG
ACCATTGCCCTCCCAAATCCCTCCAGGCCAGAACACTGACTGGAGCAGGCATGGCCACCAAG
GCTTCAGGAGTAGGGGAAGCCTGGAGCCCCACTCCAGCCCTGGGACAACTTGAGAATTCCCC
CTGAGGCCAGTCTGTCATGGATGCTGCTGAGAATAACTTGCTGTCCCGGTGTACCTGC
TTCCATCTCCAGCCACCAGCCCTCTGCCACCTCACATGCCTCCCATGGATTGGGGCCT
CCCAGGCCCCCACCCTTATGTCAACCTGCACCTTGTCAAAAATCAGGAAAAGAAAAGAT
TTGAAGACCCAAGTCTTGTCAATAACTTGCTGTGGAAGCAGCGGGGAAGACCTAGAAC
CCTTCCCCCAGCACTGGTTCCAACATGATAATTATGAGTAATTATTTGATATGTACA
TCTCTTATTTCTTACATTATTATGCCCAAATTATATTATGTATGTAAGTGAGGTTG
TTTGTATATAAATGGAGTTGTTGT

FIGURE 22

MRSGCVVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWDPIRLRHLYTSGPHGLSSCFLRI
RADGVVDCARGQSAHSLLIEIKAVALRTVAIKGVHSVRYLCMGADGKMQGLLQYSEEDCAFEE
EIRPDGYNVYRSEKHRLPVSLSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD
MFSSPLETDSMDPFGLVTGLEAVRSPSFEK

Signal peptide:

amino acids 1-22

Casein kinase II phosphorylation site.

amino acids 78-82, 116-120, 190-194, 204-208

N-myristoylation site.

amino acids 15-21, 54-60, 66-72, 201-207

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 48-59

FIGURE 23

CCCAGAAGTTCAAGGGCCCCGGCCTCTGCGCTCCTGCCGCCGGACCCCTGACCTCCTCA
GAGCAGCCGGCTGCCGCCGGAAAGATGGCGAGGAGGAGCCACCGCCCTCCTGCTG
CTGCTGCGCTACCTGGTGGTCGCCCTGGCTATCATAAGGCCTATGGGTTTCTGCCCAAA
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTAGCCTGAAAACCCAA
AGAAGACTGTTCCAGATTAGAGTGGAAAGAAACTGGGTGGAGTGTCTCCTTGCTAC
TATCAACAGACTCTCAAGGTGATTTAAAAATCGAGCTGAGATGATAGATTCAATATCCG
GATCAAAAATGTGACAAGAAGTGATGCGGGAAATATCGTTGTGAAGTTAGTGCCCCATCTG
AGCAAGGCCAAAACCTGGAAGAGGATAACAGTCACCTGGAAGTATTAGTGGCTCCAGCAGTT
CCATCATGTGAAGTACCCCTCTGCTCTGAGTGGAACTGTGGTAGAGCTACGATGTCAGA
CAAAGAAGGAAATCCAGCTCTGAATACACATGGTTAAGGATGGCATCGTTGCTAGAAA
ATCCCAGACTGGCTCCAAAGCACCAACAGCTCATACACAATGAATAACAAAAACTGGAAC
CTGCAATTAAACTGTTCCAAACTGGACACTGGAGAATATTCTGTGAAGCCGCAATT
TGTGGATATCGCAGGTGTCCTGGAAACGAATGCAAGTAGATGATCTCAACATAAGTGGCA
TCATAGCAGCCGTAGTAGTTGTGGCCTAGTGATTCCGTTGTGGCCTGGTGTATGCTAT
GCTCAGAGGAAAGGCTACTTTCAAAAGAAACCTCCCTCAGAAGAGTAATTCTCATCTAA
AGCCACGACAATGAGTGGAAATGTGCAGTGGCTCACGCCGTAAATCCAGCACTTGGAAAGG
CCGGCGGGCGGATCACGAGGTCAAGGAGTTCTAGACCAGTCTGCCAATATGGTAAACCC
CATCTCTACTAAAATACAAAAATTAGCTGGCATGGTGGCATGTGCCTGCAGTTCCAGCTGC
TTGGGAGACAGGAGAATCACTGAACCCGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGC
CACTGCAGTCCAGCCTGGTAACAGAGCAAGATTCCATCTCAAAAATAAATAAATAAATA
AATAAATACTGGTTTACCTGTAGAATTCTTACAATAATAGCTTGATATT

FIGURE 24

MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTVSSRLE
WKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEED
TVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKD GIRLLENPRLGSQST
NSSYTMNTKTGTLQFNTVSKLDTGEYSCEARN SVGYRRCPGKRMQVDDLNI SGIIIAVVVVA
LVI SVCGLGV CYAQRKGYFSKETSFQKSNSSSKATTMSENVQWLTPVIPALWKA AAGGSRGQEF

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 130-144, 238-258

N-glycosylation site.

amino acids 98-102, 187-191, 236-240, 277-281

Casein kinase II phosphorylation site.

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

N-myristoylation site.

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

Amidation site.

amino acids 226-230

FIGURE 25

GACATCGGAGGTGGCTAGCACTGAAACTGCTTTCAAGACGAGGAAGAGGAGGAGAAAGAG
AAAGAAGAGGAAGATGTTGGCAACATTATTTAACATGCTCCACAGCCGGACCTGGCAT
CATGCTGCTATTCTGCAAATACTGAAGAAGCATGGGATTAAATATTTACTTCTAAATAA
ATGAATTACTCAATCTCCTATGACCATCTACATACTCCACCTTCAAAAAGTACATCAATA
TTATATCATTAAGGAAATAGTAACCTCTCTTCCAATATGCATGACATTTGGACAATG
CAATTGTGGCACTGGCACTTATTCAGTGAAGAAAAACTTGTGGTTCTATGGCATTCA
TTTGACAAATGCAAGCATCTTCTTATCAATCAGCTCTATTGAACCTACTAGCACTGACTG
TGGATCCTTAAGGGCCATTACATTTCTGAAGAAGAAAGCTAAGATGAAGGACATGCCACT
CCGAATTCATGTGCTACTTGGCTAGCTATCACTACACTAGTACAAGCTGTAGATAAAAAAG
TGGATTGTCCACGGTTATGTACGTGTGAATCAGGCCTGGTTACACCCAGATCCATTAT
ATGGAAGCATCTACAGTGGATTGTAATGATTTAGGTCTTTAACTTCCCAGCCAGATTGCC
AGCTAACACACAGATTCTCTCCTACAGACTAACAAATTGCAAAAATTGAATACTCCACAG
ACTTTCCAGTAAACCTTACTGGCCTGGATTATCTCAAAACAATTATCTCAGTCACCAAT
ATTAATGTAAAAAAAGATGCCTCAGCTCCTTCTGTGTACCTAGAGGAAAACAAACTTACTGA
ACTGCCTGAAAAAAATGTCGTCCGAACGTGAGCAACTTACAAGAACTCTATATTAAATCACAACT
TGCTTCTACAATTTCACCTGGAGCCTTATTGGCCTACATAATCTTCTCGACTTCATCTC
AATTCAAATAGATTGCAGATGATCAACAGTAAGTGGTTGATGCTCTCCAAATCTAGAGAT
TCTGATGATTGGGGAAATCCAATTATCAGAATCAAAGACATGAACCTTAAGCCTTTATCA
ATCTCGCAGCCTGGTTAGCTGGTATAAACCTCACAGAAATACCAAGATAACGCCTTGGTT
GGACTGGAAAACCTAGAAAGCATCTCTTTACGATAACAGGGCTTATTAAAGTACCCCATGT
TGCTCTCAAAAAGTTGTAATCTCAAATTGGATCTAAATAAAATCCTATTAAATAGAA
TACGAAGGGGTGATTTAGCAATATGCTACACTTAAAGAGTTGGGATAAAATAATATGCCT
GAGCTGATTCCATCGATAGTCTGCTGGATAACCTGCCAGATTAAAGAAAATAGAAGC
TACTAACACCCCTAGATTGTCTTACATTCCCCAATGCATTTCAGACTCCCCAAGCTGG
AATCACTCATGCTGAACAGCAATGCTCTCAGTGCCTGTACCATGGTACCTGAGTCTCTG
CCAAACCTCAAGGAAATCAGCATACACAGTAACCCCATCAGGTGTACTGTGTCATCCGTTG
GATGAACATGAACAAAACCAACATTGATTCTGGAGCCAGATTCACTGTTTGCCTGGACC
CACCTGAATTCCAAGGTCAAGATGTTGGCAAGTGCATTTCAGGGACATGATGGAATTGTT
CTCCCTCTTATAGCTCCTGAGAGCTTCTTCTAATCTAAATGAGACTGGGAGCTATGT
TTCCTTCACTGTAGAGCTACTGCAAGAACACAGCCTGAAATCTACTGGATAACACCTCTG
GTCAAAAACCTTGCCTAATACCCCTGACAGACAAGTTCTATGTCCATTCTGAGGGAAACACTA
GATATAAAATGGCGTAACTCCAAAGAAGGGGTTATATACTTGTATAGCAACTAACCTAGT
TGGCGCTGACTTGAAGTCTGTTATGATCAAAGTGGATGGATCTTCCACAAGATAACAATG
GCTCTTGAATATTAAGAGATATTCAAGGCCATTCACTGGATTTGGTGTCTGGAAAGCA
AGTTCTAAAATTCTCAAATCTAGTGTAAATGGACAGCCTTGTCAAGACTGAAAATTCTCA
TGCTGCGAAAGTGCCTGAATACCATCTGATGTCAAGGTATATAATCTTACTCATCTGAATC
CATCAACTGAGTATAAAATTGTATTGATATTCCACCATCTATCAGAAAAACAGAAAAAAA
TGTGTAAATGTCACCACCAAGGTTGCACCCCTGATCAAAGAGTATGAAAAGAATAATAC
CACAAACACTTATGGCCTGTCTGGAGGCCTCTGGGGATTATTGGTGTGATATGTCTTATCA
GCTGCCTCTCCAGAAATGAACCTGTGATGGTGGACACAGCTATGTGAGGAATTACTACAG
AAACCAACCTTGCATTAGGTGAGCTTATCCTCTGTATAATCTGGGAAGCAGGAAA
AGAAAAAAAGTACATCACTGAAAGTAAAGCAACTGTTAGGTTACCAACAAATATGTCCT
AAAAACCAACCAAGGAAACCTACTCCAAAAATGAAC

FIGURE 26

MKDMPLRIHVLLGLAITTLVQAVDKVDCPRLCTCEIRPWFTPRSIYMEASTVDCNDLGLLT
FPARLPANTQILLQTNNIAKIEYSTDGPVNLTGDLISQNNLSSVTNINVKKMPQLLSVYLE
ENKLTELPEKCLSELSNLQELYINHNLLSTISPGAFIGLHNLLRLHLNSNRQMINSKWFDA
LPNLEILMIGENPIIRIKDMNFKPPLINLRSVIAGINLTEIPDNALVGLENLESISFYDNRL
IKVPHVALQKVVLNKFLDLNKNPINRIRRQDFSNMLHLKELGINNMPELISIDS LAVDNLPD
LRKIEATNNPRLSYIHPNAFFRLPKLESMLNSNALSALYHGTIESLPNLKEISIHSNPIRC
DCVIRWMNMNKTNIRFMEPDSLFCVDPPEFQGQNVRFQVHFRDMMEICLPLIAPESFPSNLNV
EAGSYVFSHCRATAEPQPEIYWITPSGQKLLPNTLTDKFYVHSEGTLINGVTPKEGGLYTC
IATNLVGADLKSVMIKVDGSPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAFV
KTENSHAAQSARI PSDVKVYNLTHLN PSTEYKICIDIPTIYQKNRKKCVN VTTKGLHPDQKE
YEKNNTTTLMACLGGLLGIIGVICLISCLSPEMNC DGGHSYVRNYLQKPTFALGELYPP LIN
LWEAGKEKSTSLKVKA TVIGLPTNMS

Signal sequence:

amino acids 1-22

Transmembrane domain:

amino acids 633-650

N-glycosylation site.

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,
608-612, 624-628, 625-629

Casein kinase II phosphorylation site.

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

Tyrosine kinase phosphorylation site.

amino acids 570-579

N-myristoylation site.

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,
491-497, 492-498, 634-640, 702-708

Cell attachment sequence.

amino acids 277-280

FIGURE 27

GCCCCGGACTGGCGCAAGGTGCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG
CTGCAGCCTTTGAAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTAC
CACGCTTGGAGTAGATGAGGAATGGGCTCGTATTGCTGACATTCCAGC**ATGA**ATCT
GGTAGACCTGTGGTTAACCGTTCCCTCTCCATGTGTCTCCTCCTACAAAGTTGTTCTTA
TGATACTGTGCTTCATTCTGCCAGTATGTGTCCAAAGGGCTGTCTTGTCTCCTCTGGG
GGTTAAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTCCTCCTGA
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCAATGAAATTAAAGG
ACCTCCATCAACTGAGAGTTCTAACCTGTCCAAAAATGGCATTGAGTTATCGATGAGCAT
GCCTTCAAAGGAGTAGCTGAAACCTTGCAACTCTGGACTTGTCCGACAATCGGATTCAAAG
TGTGCACAAAAATGCCTCAATAACCTGAAGGCCAGGGCAGAATTGCCAACACCCTGGC
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCCAC
AACGTGATCTGAAAACGTCCGTGGATGAAACATGCTGGCAGACCATTCTCAATGCTGC
CAACGACGCTGACCTTGTAACCTCCCTAAAAAAACTACCGATTATGCCATGCTGGTCACCA
TGTGTTGGCTGGTTCACTATGGTGTCTCATATGTGGTATATTATGTGAGGAAAATCAGGAG
GATGCCCGGAGACACCTCGAATACTTGAAATCCCTGCCAACGAGGAGAAGAAAGCAGATGA
ACCTGATGATATTAGCACTGTGGT**A**TAGTGTCCAAACTGACTGTCAATTGAGAAAGAAAGAAA
GTAGTTGCGATTGCACTAGAAATAAGTGGTTACTTCTCCCATCCATTGTAAACATTGAA
ACTTTGTATTCAGTTTTTGAAATTATGCCACTGCTGAACTTAACAAACACTACAACA
TAAATAATTGAGTTAGGTGATCCACCCCTTAATTGTACCCCCGATGGTATATTCTGAGT
AAGCTACTATCTGAACATTAGTTAGATCCATCTCACTATTAAATAATGAAATTATTTTT
AATTAAAAGCAAATAAAAGCTTAACTTGAACCATGGAAAAAAAAAAAAAAACA

FIGURE 28

MNLVDLWLTRSLSMCLLLQSFVLMILCFHSASMC PKGCLSSSGGLNVTC SANLKEIPRDL
PPETVLLYLDNSNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTLDLSDNR
IQSVHKNAFNNLKARARIANNPWHCDCTLQQVLRSMASNHETAHNICKTSVLDEHAGR PFL
NAANDADLCNLPKKTTDYAMLVTMFGWFTMVISYVVYYVRQNQEDARRHLEYLKSLPSRQKK
ADEPDDISTVV

Signal sequence:

amino acids 1-33

Transmembrane domain:

amino acids 205-220

N-glycosylation site.

amino acids 47-51, 94-98

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 199-203

Casein kinase II phosphorylation site.

amino acids 162-166, 175-179

N-myristoylation site.

amino acids 37-43, 45-51, 110-116

FIGURE 29

ACCGAGCCGAGCGGACCGAAGGCAGCAGATGAGGTGAGCAAGAGGATGCTGGCGGGG
GGCGTGAGGAGCATGCCAGCCCCCTCCTGGCTGGCAGCCCATTCTCTGCTGGTGTCT
GGGCTCAGTGCTGTCAAGGCTCGGCCACGGCTGCCGCCCCGCTGCGAGTGCTCCGCCAGG
ACCGCGCTGTGCTGTGCCACCGCAAGTGCTTTGTGGCAGTCCCCGAGGGCATCCCCACCGAG
ACGCGCCTGCTGGACCTAGGAAGAACCGCATAAAACGCTCAACCAGGACGGAGTCGCCAG
CTTCCCACCTGGAGGAGCTGGAGCTCAACGAGAACATCGTAGCGCCGTGGAGGCCCGCG
CCTTCACAAACACTCTCACCTCCGGACGCTGGGTCTCCGCAGCAACGCCCTGAAGCTCATC
CCGCTAGGCCTTCACTGGCCTCAGAACCTGACCAAGCAGGACATCAGCGAGAACAGAT
CGTTATCCTACTGGACTACATGTTCAGGACCTGTACAACCTCAAGTCACTGGAGGTGGCG
ACAATGACCTCGTCTACATCTCACCGCGCCTCAGCGCCTCAACAGCCTGGAGCAGCTG
ACGCTGGAGAAATGCAACCTGACCTCCATCCCCACCGAGGGCTGTCCCACCTGCACGGCCT
CATCGTCCCTGAGGCTCCGGCACCTCAACATCAATGCCATCCGGACTACTCCTCAAGAGGC
TGTACCGACTCAAGGTCTGGAGATCTCCACTGGCCCTACTTGGACACCATGACACCCAAC
TGCCTCTACGCCCTCACCTGACGTCCCTGTCCATCACACACTGCAATCTGACCGCTGTGCC
CTACCTGGCCGTCCGCCACCTAGTCTATCTCGCTTCTCACCTCTCACACCCATCA
GCACCAATTGAGGGCTCCATGTTGATGAGCTGCTCCGGCTGCAGGAGATCCAGCTGGGGC
GGGCAGCTGGCGTGGTGGAGCCCTATGCCCTCCGCCCTCAACTACCTGCGCGTGTCAA
TGTCTCTGGCAACCAGCTGACCAACTGGAGGAATCAGTCTTCACTCGGTGGCAACCTGG
AGACACTCATCTGGACTCCAACCCGCTGGCTGCGACTGTCGGCTCCTGTGGGTGTCCGG
CGCCGCTGGCGGCTCAACTCAACCGGAGCAGGCCACGTGCCACGCCAGTTGTCCA
GGGCAAGGAGTTCAAGGACTTCCCTGATGTGCTACTGCCAACTACTTCACCTGCCGCCGCG
CCCCGATCCGGGACCGCAAGGCCAGCAGGTGTTGTGGACGAGGCCACACGGTGCAGTT
GTGTGCCGGGGCATGGCACCAGCCGCCATCCTCTGGCTCTCACCCGAAAGCACCT
GGTCTCAGCCAAGAGCAATGGCGGCTCACAGTCTCCCTGATGGCACGCTGGAGGTGCGCT
ACGCCAGGTACAGGACAACGGCACGTACCTGTGCATCGGGCAACGCCGGCAACGAC
TCCATGCCGCCACCTGCATGTGCGCAGCTACTGCCGACTGGCCCCATAGCCAAACAA
GACCTCGCTTCATCTCAACCAGCCGGCGAGGGAGAGGCCAACAGCACCGGCCACTG
TGCCTTCCCTCGACATCAAGACCTCATCATGCCACCACATGGGCTCATCTCTTTC
CTGGCGTGTCCCTCTGCCCTGGTGTGCTGTTCTGGAGCCGGGCAAGGGAACAC
AAAGCACAAACATCGAGATCGAGTATGTGCCCAAAGTCGGACGCAGGCATCAGCTCCGCCG
ACGCCGCCGCAAGTTCAACATGAAGATGATTGAGGCCGGGCGGGGGCAGGGACCCCG
GGCGCCGGGAGGGGCTGGTCGCCACCTGCTCACTCTCAGTCCTTCCACCT
CTCCCTACCCCTCTACACACGTTCTTCTCCCTCCGCCCTCCGTCCCCTGCTGCCCG
CCAGCCCTACCCACCTGCCCTCTTCTACCGAACCTCAGAACGCCAGACCTGGGGACCCCA
CCTACACAGGGGATTGACAGACTGGAGTTGAAAGCCGACGAACCGACACGCCAGAGTC
ATAATTCAATAAAAAGTTACGAACCTTCTCTGTAACCTGGTTCAATAATTATGGATTT
TATGAAAACTTGAAATAATAAAAAGAGAAAAAAACTAAAAAAAAAAAAAA

FIGURE 30

MQVSKRMLAGGVRSMPSPLLACWQPILLVLGSVLSGSATGCPPCECSAQDRAVLCHRKCF
VAVPEGIPTETRLLDLGKNRIKTLNQDEFASFPHLEELENENIVSAVEPGAFNNLFNLRTL
GLRSNRKLIPLGVFTGLSNLTKQDISENKIVILLDYMFQDLYNLKSLEVGDNDLVYISHRA
FSGLNSLEQLTLEKCNLTSIPTEALSHLHGLIVLRLRHLMINAIRDYSFKRLYRLKVLEISH
WPYLDTMTPNCLYGLNLTSLSITHCNLTAVPYLAVRHLVYLRFLNLSYNPISTIEGSMLHEL
LRLQEIQLVGGQLAVVEPYAFRGLNYLRVNVSGNQLTLEESVFHSVGNLLETLILDSENPLA
CDCRLLWVFRWRNLNFNRQQPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQV
FVDEGHTVQFVCRADGDPPIALWLSPRKHLVSAKSNGRLTVFPDGTLLEVRYAQVQDNGTYL
CIAANAGGNDSMPAHLHVRSYS PDWPHQPNKTFAFISNQPGEGEANSTRATVPFPFDIKTLI
IATTMGFISFLGVVLFCLVLLFLWSRGKGNTKHNIEIEYVPRKSDAGISSADAPRKFNMKMI

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 556-578

N-glycosylation site.

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,
492-496, 505-509, 526-530, 542-546

Casein kinase II phosphorylation site.

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,
607-611

Tyrosine kinase phosphorylation site.

amino acids 590-598

N-myristoylation site.

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 32-43

FIGURE 31

CCCAACGCGTCCGCACCTCGGCCCGGGCTCCGAAGCGGCTCGGGGGCGCCCTTCGGTCAAC
ATCGTAGTCCACCCCCTCCCCATCCCCAGCCCCGGGGATTCAAGGCTGCCAGGCCAGCC
AGGGAGCCGGCCGGGAAGCGCGATGGGGCCCCAGCCGCCTCGCTCCTGCTCCTGC
TGTTCGCCTGCTGCTGGCGCCCGGGCAACCTCTCCCAGGACGACAGCCAGCCCTGG
ACATCTGATGAAACAGTGGTGGCTGGCACCGTGGTCAAGTCCAAGTGAAAGATCA
CGAGGACTCATCCCTGCAATGGCTAACCTGCTCAGCAGACTCTACTTGGGAGAAGA
GAGCCCTTCGAGATAATCGAATTCACTGGTTACCTCTACGCCAACGAGCTCAGCATCAGC
ATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTTCACTATGCCGT
GCGAACTGCCAAGTCCCTCGTCACTGTGCTAGGAATTCCACAGAACGCCATCATCACTGGTT
ATAAATCTTCATTACGGGAAAAAGACACAGCCACCCCTAAACTGTCAGTCTTCTGGGAGCAAG
CCTGCAGCCCCGGCTCACCTGGAGAAAGGGTACCAAGAACTCCACGGAGAACCAACCGCAT
ACAGGAAGATCCCAATGGTAAAACCTTCACTGTCAGCAGCTCGGTGACATTCCAGGTTACCC
GGGAGGGATGATGGGGCGAGCATCGTGTGCTCTGTGAACCAGTAAAGGGAGCTGAC
AGATCCACCTCTCAACGCATTGAAGTTTATACACACCAACTGCGATGATTAGGCCAGACCC
TCCCCATCCTCGTGAGGGCCAGAAGCTGTTGCTACACTGTGAGGGTCGCGCAATCCAGTCC
CCCAGCAGTACCTATGGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT
GCCCTGATCTTCCCTTCCTCAACAAGAGTGACAGTGGCACCTACGGCTGCACAGCCACCAG
CAACATGGGAGCTACAAGGCCTACTACACCCCTCAATGTTAATGACCCAGTCCGGTCCCT
CCTCCTCCAGCACCTACCAACGCCATCATCGTGGATCGTGGCTTCATTGTCTCCTGCTG
CTCATCATGCTCATCTCCTTGCCACTACTTGATCCGGCACAAAGGAACCTACCTGACACA
TGAGGCAAAAGGCTCCGACGATGCTCCAGACGGACACGGCATCATCAATGCAGAAGGCG
GGCAGTCAGGAGGGGACGACAAGAAGGAATATTCATAGAGGCGCCTGCCACTTCTGC
GCCCCCAAGGGGCCCTGTGGGACTGCTGGGCCGTACCAACCCGGACTTGTACAGAATGTCTGC
CCGCAGGGCCGCCCTCCGCTTGCTCCCCAGCCCACCCACCCCTGTACAGAATGTCTGC
TTTGGGTGCGGTTTGACTCGGTTGGAATGGGGAGGGAGGAGGGCGGGGGAGGGAGGG
TTGCCCTCAGCCCTTCCGTGGCTCTGCATTGGTTATTATTATTTGTAACAATCC
CAAATCAAATCTGTCTCCAGGCTGGAGAGGCAGGAGGCCCTGGGTGAGAAAAGCAAAAACA
AACAAAAAACA

FIGURE 32

MGAPAASLLLLLFAACCWAPGGANLSQDDSQWPWTSDETVVAGGTVVLKCQVKDHEDSSLQW
SNPAQQTLYFGEKRALRDNRIQLVTSTPHELSIISNVALADEGEYTCISIFTMPVRTAKSLV
TVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGK
TFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ
KLLLHCEGRGNPVPQQYLWEKEGSVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKA
YYTLNVNDPSPVPSSSSTYHAIIGGIVAFIVFLLIMLIFLGHYLIRHKGTYLTHEAKGSDD
APDADTAIINAEGGQSGGDDKKEYFI

Signal sequence:

amino acids 1-20

Transmembrane domain:

amino acids 331-352

N-glycosylation site.

amino acids 25-29, 290-294

Casein kinase II phosphorylation site.

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

N-myristoylation site.

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,
306-310, 334-340, 360-364, 385-389, 386-390

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 33

GGGGGTTAGGGAGGAAGGAATCCACCCCCCACCCCCCCTTCAACCCCTTCTTCCTTCTGG
CTTCGGACATTGGAGCACTAAATGAACTTGAATTGTGTCGTGGCGAGCAGGATGGTCGCTG
TTACTTTGTGATGAGATCGGGATGAATTGCTCGCTTAAAATGGCTGCTTGGATTCTGTT
GCTGGAGACGTCTTTGCTGGAAACGTTACAGGGACGTTGCAAAGAGAAGA
TCTGTTCTGCAATGAGATAGAAGGGACCTACACGTAGACTGTGAAAAAAAGGGCTTCACA
AGTCTGCAGCGTTCACTGCCCGACTTCCCAGTTTACCATTTATTCTGCATGGCAATT
CCTCACTCGACTTTCCCTAATGAGTCGCTAACCTTATAATGCCGTTAGTTGCACATGG
AAAACAATGGCTTGCAATGAAATCGTCCGGGGCTTTCTGGGCTGCAGCTGGTAAAAGG
CTGCACATCAACAACAAGATCAAGTCTTCGAAAGCAGACTTTCTGGGCTGGACGA
TCTGGAATATCTCCAGGCTGATTTAATTATTACGAGATATAGACC CGGGCCTCCAGG
ACTTGAACAAGCTGGAGGTGCTCATTTAAATGACAATCTCATCAGCACCCCTACCTGCCAAC
GTGTTCCAGTATGTGCCATCACCCACCTCGACCTCCGGGTAACAGGCTGAAAACGCTGCC
CTATGAGGAGGTCTTGAGCAAATCCCTGGTATTGCGGAGATCCTGCTAGAGGATAACCCTT
GGGACTGCACCTGTGATCTGCTCCCTGAAAGAATGGCTGGAAAACATTCCAAGAATGCC
CTGATCGGCCAGTGGCTGCGAAGCCCCCACAGACTGCAGGGTAAAGACCTCAATGAAAC
CACCGAACAGGACTTGTGTCCTTGAAACCGAGTGGATTCTAGTCTCCGGCGCCCCCTG
CCCAAGAACAGACCTTGCTCTGGACCCCTGCCAACCTCCCTCAAGACAAATGGCAAGAG
GATCATGCCACACCAGGGCTGCTCCAAACGGAGGTACAAAGATCCCAGGCAACTGGCAGAT
CAAAATCAGACCCACAGCAGCGATAGCGACGGTAGCTCAGGAACAAACCTTAGCTAAC
GTTTACCTGCCCTGGGGCTGCGAGCTGCGACCATCCCAGGGTGGTTAAAGATGAAC
TGCAACAACAGGAACGTGAGCAGCTGGCTGATTGAAGCCAAGCTCTAACGTGCAGGA
GCTTTCCCTACGAGATAACAAGATCCACAGCATCCGAAATCGACTTGTGGATTACAAGA
ACCTCATTCTGTGATCTGGCAACAATAACATCGCTACTGTAGAGAACAAACACTTCAAG
AACCTTTGGACCTCAGGTGGCTATACATGGATAGCAATTACCTGGACACGCTGTCCGG
GAAATTCGCGGGCTGCAAAACCTAGAGTACCTGAACGTGGAGTACAACGCTATCCAGCTCA
TCCTCCGGGCACTTCAATGCCATGCCAAACTGAGGATCCTCATTCTAACAAACAACCTG
CTGAGGTCCCTGCCTGGACGTGTTGCTGGCTCTCTAAACTCAGCCTGCACAA
CAATTACTCATGTACCTCCGGTGGCAGGGTGTGGACCAGTTAACCTCCATCATCCAGA
TAGACCTCCACGGAAACCCCTGGGAGTGTCTGCACAATTGTGCCTTCAAGCAGTGG
GAACGCTGGGTTCCGAAGTGTGATGAGCGACCTCAAGTGTGAGACGCCGGTGAACCT
TAGAAAGGATTTCATGCTCCTCCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCT
CGCCCACGTTAACCTCGCACAGTAAAACAGCACTGGGTGGCGAGACGGGACGCACTCC
AACTCCTACCTAGACACCAGCAGGGTGTCCATCTCGGTGGTCCGGACTGCTGCTGGT
GTTTGTACCTCCGCCCTCACCGTGGGGCATGCTCGTGTGTTATCCTGAGGAACCGAAAGC
GGTCCAAGAGACGAGATGCCAACTCCTCCGCGTCCGAGATTAATTCCCTACAGACAGTCTG
GACTCTCCTACTGGCACAAATGGGCTTACAACGCAGATGGGCCACAGAGTGTATGACTG
TGGCTCTACTCGCTCAGACTAAAGACCCCAACCCCAATAGGGAGGGCAGAGGGAAAGGCG
ATACATCCTCCCCACCGCAGGCACCCGGGGCTGGAGGGCGTGTACCCAAATCCCGCG
CCATCAGCCTGGATGGGCATAAGTAGATAAAACTGTGAGCTGCACAAACGAAAGGGCT
GACCCCTACTTAGCTCCCTCCTGAAACAAAGAGCAGACTGTGGAGAGCTGGAGAGCGCA
GCCAGCTCGCTTTGCTGAGAGCCCCTTGACAGAAAGCCAGCACGACCCCTGCTGGAAG
AACTGACAGTGCCTCGCCCTGGCCCGGGCTGTGGGGTTGGATGCCGGTTCTATAC
ATATATACATATCCACATCTATATAGAGAGATAGATATCTATTCCCTGTGGATTAG
CCCCGTGATGGCTCCCTGTTGGCTACGCAGGGATGGCAGTTGCACGAAGGCATGAATGTAT
TGTAAATAAGTAACCTTGACTTCTGAC

FIGURE 34

MLLWILLLETSLCFAAGNVTGVCCKEKCSCNEIEGDLHVDCCEKKGFTSLQRFTAFTSQFYH
LFLHGNSLTRLFPNEFANFYNAVSLHMENGLHEIVPGAFGLQLVKRLHINNNKIKSFRKQ
TFLGLDDLEYLQADFNLLRDIDPGAFQDLNKLEVILNDNLISTLPANVFQYVPITHLDLRG
NRLKTLPYEEVLEQIPGIAEILLEDPNPWDCTCDLLSLKEWLENIPKNALIGRVVCEAPTRLQ
GKDLNNETTEQDLCPLKNRVDSSLAPPAPPAQEETFAPGPLPTPKTNGQEDHATPGSAPNGGT
IPGNWQIKIRPTAAIATGSSRNKPLANSLPCPGGCSCDHIPGSGLKMNCNNRNVSSLADLKP
KLSNVQELFLRDNKIHSIRKSHFDYKNLILLDLGNNNIATVENNTFKNLLDLRWLYMDSNY
LDTLSREKFAGLQNLEYLNVEYNIAIQILIPGTFNAMPKLRILILNNNLLRSILPVDVFAGVSL
SKLSLHNYYFMYLPVAGVLDQLTSIIQIDLHGNPWECSCTIVPKQWAERLGSEVLMSDLKC
ETPVNFFRKDFMLLSNDEICPQLYARISPTLTSHSKNSTGLAETGTHNSYLDTSRVSISVL
VPGLLLGVFTSAFTVVGMLVFIIRNRKRSKRRDANSASEINSLQTVCDSYWHNGPYNADG
AHRVYDCGSHSLSD

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 618-638

N-glycosylation site.

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 122-126, 646-650

Casein kinase II phosphorylation site.

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,
608-612, 657-661, 666-670, 693-697

N-myristoylation site.

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,
354-360, 465-471, 493-499, 598-604, 603-609

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 337-348

FIGURE 35

AGTCGACTGCGTCCCCGTACCCGGCGCAGCTGTGTTCTGACCCCAGAATAACTCAGGGC
TGCACCGGGCCTGGCAGCGCTCCGACACATTCTGTGCGGGCCTAAGGGAAACTGTTGGC
CGCTGGGCCCGGGGGATTCTTGGCAGTTGGGGGTCCCGTCGGGAGCGAGGGCGGAGGG
AAGGGAGGGGAACCAGGGTTGGGAAGCCAGCTGTAGAGGGCGGTGACCGCGCTCCAGAAC
AGCTCTGCGTCCTCGAGCGGACAGATCCAAGTTGGGAGCAGCTCTGCGTGCAGGGCCTCAG
AGAATGAGGCCGGCGTTGCCCTGTGCCTCCTCTGGCAGGGCGCTCTGGCCCGGGCGG
CGCGAACACCCACTGCCGACCGTGCTGGCTGCTCGGCCTCGGGGGCTGCTACAGCCTGC
ACCACGCTACCATGAAGCGGCAGGCAGGAGGAGGCCTGCATCCTGCGAGGTGGGCGCTC
AGCACCGTGCCTGGGGCGCCGAGCTGCAGCTGTGCTCGCGCTCTGCGGGAGGCCAGG
GCCCGAGGGGCTCAAAGACCTGCTGTTCTGGGTCGCACTGGAGCGCAGGCAGTCCCAGT
GCACCCCTGGAGAACAGAGCCTTGCGGGGTTCTCCTGGCTGTGCTCCGACCCGGCGGTCTC
GAAAGCGACACGCCAGCTGCAGTGGGTGGAGGAGGCCAACGCTCCTGCAACCGCGAGATGCGC
GGTACTCCAGGCCACCAGTGGGGTCGAGCCGCAGGCTGGAAGGAGATGCGATGCCACCTGC
GCGCCAACGGCTACCTGTCAAGTACCAAGTGGAGGCTTGAGGTCTTGTGTCCTGCGCCGCCGG
GCCGCTCTAACCTGAGCTATCGCGCCCTTCCAGCTGCACAGCGCCGCTCTGGACTTCAG
TCCACCTGGGACCGAGGTGAGTGCCTCTGCCGGGACAGCTCCGATCTCAGTTACTTGCA
TCGCGGACGAAATCGGCGCTCGCTGGGACAAACTCTCGGGCGATGTGTTGTCCTGCC
GGGAGGTACCTCCGTCTGGCAAATGCGCAGAGCTCCCTAAGTGCCTAGACGACTTGGGAGG
CTTGCCCTGCAATGTGCTACGGGCTTCGAGCTGGGGAGGACGGCCGCTCTGTGACCA
GTGGGAAGGACAGCGACCCCTGGGGGACCGGGTGCCCACCAGCGCCGCCACT
GCAACCAGCCCGTGCAGAGAACATGGCAATCAGGGTCGACGAGAACGACTGGGAGAGAC
ACCACTGTCCCTGAACAAGACAATTCAAGTAACATCTATTCTGAGATTCTCGATGGGAT
CACAGAGCACGATGTCTACCCCTCAAATGTCCTCAAGCCGAGTCAAAGGCCACTATCACC
CCATCAGGGAGCGTGATTCCAAGTTAATTCTACGACTTCTCTGCCACTCTCAGGCTT
CGACTCCCTCTGCCGTGGTCTTCATATTGTGAGCACAGCAGTAGTGTGTTGGTGTCT
TGACCATGACAGTACTGGGCTTGTCAAGCTCTGCTTCAAGAAAGCCCTCTCCAGCCA
AGGAAGGAGTCTATGGGCCGCCGGCTGGAGAGTGTCTGAGCCGCTGTTGGGCTC
CAGTTCTGCACATTGCACAAACATGGGGTCAAAGTCGGGACTGTGATCTGGGACAGAG
CAGAGGGTGCCTTGTGGCGAGTCCCTTGGCTCTAGTGATGCATAGGGAAACAGGGGA
CATGGGCACTCCTGTGAACAGTTTCACTTTGATGAAACGGGGACCAAGAGGAACCTAC
TTGTGTAACGTACAATTCTGCAGAAATCCCCCTTCTCAAATTCCCTTACTCCACTGAG
GAGCTAAATCAGAACTGCACACTCCTCCCTGATGATAGAGGAAGTGGAAAGTGCCTTAGGA
TGGTGATACTGGGGACGGTAGTGCTGGGAGAGATATTCTTATGTTATTGGAGAA
TTGGAGAAGTGTGAACTTTCAAGACATTGGAAACAAATAGAACACAATATAATTACA
TTAAAAAAATAATTCTACCAAAATGGAAAGGAAATGTTCTATGTTGTCAGGCTAGGAGTAT
ATTGGTTGAAATCCCAGGGAAAAAAATAAAAATTAAGGATTGTTGAT

FIGURE 36

MRPAFALCLLWQALWP GP GGGHPTADRAGCSASGACYSLHHATMKRQAAEEACILRGGALS
TVRAGAELRAVLALLRAGPGPGGGSKDLLFWVALERRSHCTLENEPLRGFSWLSSDPGGL
SDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYCKYQFEVLCAPRPG
ASNLSYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIADEIGARWDKLSGDVLCPCPG
RYLRAGKCAELPNCLDDLGGFACECATGFELGKDGRSCVTSGEQPTLGGTGVPTRRPPATA
TSPVPQRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITP
SGSVISKFNSTTSSATPQAFDSSAVVFIFVSTAVVVLVILMTVLGLVKLCFHESPSSQPR
KESMGPPGLESDPEPAALGSSSAHTNNGVKGDCDLRDRAEGALLAESPLGSSDA

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 189-193, 381-385

Glycosaminoglycan attachment site.

amino acids 289-293

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 98-102, 434-438

Casein kinase II phosphorylation site.

amino acids 275-279, 288-292, 342-346, 445-449

N-myristoylation site.

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,
477-483

Aspartic acid and asparagine hydroxylation site.

amino acids 262-274

FIGURE 37

CGGACGGTGGATTCAAGCAGTGGCTGGCTGCCAGAGCAGCTCCTCAGGGAAACTAAG
CGTCGAGTCAGACGGCACCATAATGCCTTAAAGTGCCTCCGCCCTGCCGGCGGTATC
CCCCGGCTACCTGGGCCCGCGCGGTGCGCGCGTGAAGAGGGAGCGCGGGCAGCCGA
GCGCCGGTGTGAGCCAGCGCTGCCAGTGTGAGCGCGGTGTGAGCGCGGTGGTGCAGA
GGGGCGTGTGCGCGCGCGCGTGGGTGCAAACCCCGAGCGTCTACGCTGCCATGA
GGGGCGCGAACGCCTGGCGCCACTCTGCCTGCTGGTGCAGCCACCCAGCTCGCGG
CAGCAGTCCCAGAGAGACCTGTTTACATGTGGTGGCATTCTACTGGAGAGTCTGGATT
TATTGGCAGTGAAGGTTTCTGGAGTGTACCCCTCCAATAGCAAATGTACTTGGAAAATCA
CAGTCCCAGAGGAAAAGTAGTCGTTCTCAATTCCGATTCAAGACCTCGAGAGTGACAAC
CTGTGCCGCTATGACTTGTGGATGTGTACAATGGCATGCCAATGGCAGCGATTGGCG
CTTCTGTGGCACTTCCGGCTGGAGCCCTGTGTCCAGTGGCAACAAGATGATGGTGCAGA
TGATTCTGATGCCAACACAGCTGGCAATGGCTCATGGCATGTTCTCCGCTGCTGAACCA
AACGAAAGAGGGATCAGTATTGTGGAGGACTCCTGACAGACCTCCGGCTTTAAAAC
CCCCAACTGGCCAGACGGGATTACCCCTGCAGGAGTCACCTGTGTGGCACATTGTAGCCC
CAAAGAATCAGCTTATAGAATTAAAGTTGAGAAGTTGATGTGGAGCGAGATAACTACTGC
CGATATGATTATGTGGCTGTGTTAATGGCGGGAAAGTCAACGATGCTAGAAGAATTGGAAA
GTATTGTGGTGTAGTCCACCTGCGCCAATTGTGTCTGAGAGAAATGAACTTCTTATTCACT
TTTATCAGACTTAAGTTAACTGCAGATGGTTATTGGTCACTACATATTCAAGGCCAAA
AAACTGCCTACAACACAGCCTGTCACCACATTCCCTGTAACCACGGTTAAA
ACCCACCGTGGCCTTGTCAACAAAAGTGTAGACGGACGGGACTCTGGAGGGCAATTATT
GTTCAAGTGACTTGTATTAGCCGGCACTGTTATCACAACCATCACTCGCGATGGAGTTG
CACGCCACAGTCTCGATCATCAACATCTACAAAGAGGGAAATTGGCGATTCAAGCAGCGGG
CAAGAACATGAGGCCAGGCTGACTGTCGTCGCAAGCAGTGCCTCTCCTCAGAACAGC
TAAATTACATTATTATGGCCAAGTAGGTGAAGATGGCGAGGCAAATCATGCCAACAGC
TTTATCATGATGTTCAAGACCAAGAACATAGAACGCTCTGGATGCCCTAAAAAATAAGCAATG
TTAAACAGTGAACGTGTCCTTAAGCTGTATTGCAATTGCCATTGCCATTGAAAGATCTATGTT
TCTCAGTAGAAAAAAATACTTATAAAATTACATATTCTGAAAGAGGATTCCGAAAGATGG
GACTGGTTGACTCTTCACATGATGGAGGTATGAGGCCCTCGAGATAGCTGAGGGAAAGTTCTT
TGCCTGCTGTCAAGAGGAGCAGCTATCTGATTGGAAACCTGCGACTTAGTGCAGGTGATAGGA
AGCTAAAAGTGTCAAGCGTTGACAGCTTGAAGCGTTATTATACATCTGTAAAGGAT
ATTTAGAATTGAGTTGTGAAGATGTCAAAAAAGATTTAGAAGTGCATATTATAGT
GTTATTGTTCACCTCAAGCCTTGCCCTGAGGTGTTACAATCTGTCTGCGTTCTA
AATCAATGCTTAATAAAATATTAAAGGAAAAAA

FIGURE 38

MRGANAWAPLCLLLAAATQLSRQQSPERPVFTCGGILTGESGFIGSEGFPGVYPPNSKCTWK
ITVPEGKVVLNFRFIDLESNDNLCRYDFVDVYNGHANGQRIGRFCGTFRPGALVSSGNKMMV
QMISDANTAGNGFMAMFSAAEPNERGDQYCGGLLDRPSGSFKTPNWPDRTDYPAGVTCVWHIV
APKNQLIELKFEKFDVERDNYCRYDYVAVFNGGEVNDARRIGKYCGDSPAPIVSERNELLI
QFLSDLSLTADGFIGHYIFRPKKLPTTTEQPVTTFPVTTGLKPTVALCQQKCRRTGTLEGN
YCSSDFVLAGTVITTITRDGSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLRR
GLNYIIMGQVGEDGRGKIMPNSFIMMFKTKNQKLDAKKNQC

Signal sequence:

amino acids 1-23

N-glycosylation site.

amino acids 355-359

Casein kinase II phosphorylation site.

amino acids 64-68, 142-146, 274-278

Tyrosine kinase phosphorylation site.

amino acids 199-208

N-myristoylation site.

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,
305-311, 309-315, 320-326, 330-336

Cell attachment sequence.

amino acids 149-152

FIGURE 39

CGGACGCGTGGCGGACGCGTGGCGGCCACGGCGCCCGGGCTGGGGCGGTGCCTTCTT
CCTCTCGTGGCTACGAGGGTCCCCAGCCTGGTAAAGAATGGCCCCATGGCCCCGAAGG
GCCTAGTCCCAGCTGTGCTCTGGGCCTCAGCCTCTTCCTCAACCTCCCAGGACCTATCTGG
CTCCAGCCCTCTCCACCTCCCCAGTCTTCTCCCCGCCTCAGCCCCATCCGTGTACACCTG
CCGGGGACTGGTTGACAGCTTAACAAGGGCTGGAGAGAACCATCCGGACAACTTGGAG
GTGGAAACACTGCCTGGAGGAAGAGAATTGTCAAATACAAAGACAGTGAGACCCGCCTG
GTAGAGGTGCTGGAGGGTGTGCAGCAAGTCAGACTTCGAGTGCCACCGCCTGCTGGAGCT
GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTACAAGCAGCAGGAGGCCCCGGACCTCTTCC
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCGCAGGCACCTCGGGCCCTCCTGC
CTTCCCTGTCTGGGGAACAGAGAGGGCCCTGCCTGGCTACGGGCAGTGTGAAGGAGAAGG
GACACGAGGGGGCAGCGGGCACTGTGACTGCCAAGCGGCTACGGGGTGAGGCCTGTGGCC
AGTGTGGCCTGGCTACTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTGGCTTGT
TTTGGCCCCGTGCCGATGCTCAGGACCTGAGGAATCAAACGTGTTGCAATGCAAGAAGGG
CTGGGCCCTGCATCACCTCAAGTGTAGACATTGATGAGTGTGGCACAGAGGGAGCCA
ACTGTGGAGCTGACCAATTCTGCGTGAACACACTGAGGGCTCCTATGAGTGCCGAGACTGTGCCAAG
GCCTGCCTAGGCTGCATGGGGCAGGGCCAGGTGCGCTGTAAGAAGTGTAGCCCTGGCTATCA
GCAGGTGGCTCCAAGTGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTCCGGAGAGA
ACAAGCAGTGTAAAACACCGAGGGCGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAG
ATGGAAGGCATCTGTGTGAAGGAGCAGATCCCAGAGTCAGCAGGCTTCTTCAGAGATGAC
AGAAGACGAGTTGGTGGTGTGCAGCAGATGTTGGCATCATCTGTGCACTGGCCA
CGCTGGCTGCTAAGGGCACTGGTGTTCACCGCCATCTCATTGGGCTGTGGCGGCCATG
ACTGGCTACTGGTTGTCAGAGCGCAGTGACCGTGTGCTGGAGGGCTTCATCAAGGGCAGA
ATCGCGCACCACTGAGCTCCTCCCACCAGGCTTGGCTG
TCCTGCTGGACACTCAGGACAGCTGGTTATTGGTAAAGTGGGTAAGCACCCTACCTG
CCTACAGAGCAGCCCAGGTACCCAGGCCGGCAGACAAGGCCCTGGGTAAAAAGTAGC
CCTGAAGGTGGATACCATGAGCTTCACTGGCGGGACTGGCAGGCTTCACAATGTGTGA
ATTCAAAAGTTTCTTAATGGTGGCTGCTAGAGCTTGGCCCTGCTTAGGATTAGGTG
GTCCTCACAGGGTGGGCCATCACAGCTCCCTGCCAGCTGCATGCCAGTTCTGT
TCTGTGTTACCACATCCCCACACCCATTGCCACTTATTATTCATCTCAGGAAATAAGA
AAGGTCTGGAAAGTTAAAAAAAAAAAAAA

FIGURE 40

MAPPPKGVLPAVLWGLSLFLNLP GPIWLQPSPPPQQSSPPPQPHPCHTCRGLVDSFNKGLER
TIRDNFGGGNTAWEENLSKYDSETRLVEVLEGVCSKSDFECHRLLESELVESWWFHKQ
QEAPDLFQWLCSDSLKLCCPAGTFGPSCLPCCPGTERPCGGYGCCEGTRGGSGHCDCQAG
YGEACGQCGLGYFEAERNASHLVCASF GPCARCSGPEESNLQCKKGWALHHLKCVDIDE
CGTEGANCGADQFCVNTEGSYECRDCAKACLGCAGAGPGRKKCSPGYQQVGSKCLDVDECE
TEVCPGENKQCENTEGGYRCICAEGYKQM EGICVKEQIPESAGFFSEMTEDELVVLQQMFFG
IIICALATLAAGDLVFTAIFIGAVAAMTGYWL SERSDRVLEGFIKGR

Signal sequence:

amino acids 1-29

Transmembrane domain:

amino acids 372-395

N-glycosylation site.

amino acids 79-83, 205-209

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 290-294

Casein kinase II phosphorylation site.

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

N-myristoylation site.

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,
326-332, 372-378, 395-401

Aspartic acid and asparagine hydroxylation site.

amino acids 321-333

EGF-like domain cysteine pattern signature.

amino acids 181-193

FIGURE 41

TGAGACCCTCCTGCAGCCTCTCAAGGGACAGCCCCACTCTGCCCTTGCTCCCTCCAGGGCA
GCACCATGCAGCCCCCTGTGGCTCTGCTGGGCACTCTGGGTGTTGCCCTGCCAGCCCCGGG
GCCGCCCTGACCGGGGAGCAGCTCCTGGCAGCCTGCTGCCAGCTGCAGCTCAAAGAGGT
GCCCACCCCTGGACAGGGCCGACATGGAGGAGCTGGTCACTCCCACCCACGTGAGGGCCCAGT
ACGTGGCCCTGCTGCAGCGCAGCCACGGGACCGCTCCCGCGAAAGAGGTTCAGCCAGAGC
TTCCGAGAGGTGGCCGGCAGGTTCTGGCGTTGGAGGCCAGCACACACCTGCTGGTTCAGG
CATGGAGCAGCGCTGCCGCCAACAGCGAGCTGGTGCAGGCCGTGCTGCCCTTCCAGG
AGCCGGTCCCCAAGGCCGGCTGCACAGGCACGGGCGGCTGTCCCCGCGAGGCCCGGGCC
CGGGTACCGTCGAGTGGCTGCCGTCCGACGACGGCTCCAACCGCACCTCCATCGA
CTCCAGGCTGGTGTCCGTCCACGAGAGCGGCTGGAAGGCCTTCGACGTGACCGAGGCCGTGA
ACTTCTGGCAGCAGCTGAGCCGGCCCCGGCAGCCGCTGCTGCTACAGGTGTCGGTGCAGAGG
GAGCATCTGGGCCCGCTGGCGTCCGGCCACAAGCTGGTCCGCTTGCCTCGCAGGGGC
GCCAGCCGGCTGGGGAGCCCCAGCTGGAGCTGCACACCCCTGGACCTGGGACTATGGAG
CTCAGGGCGACTGTGACCCCTGAAGCACCAATGACCGAGGGCACCGCTGCCGCCAGGAG
ATGTACATTGACCTGCAGGGATGAAGTGGGCCGAGAACTGGGTGCTGGAGCCCCGGGCTT
CCTGGCTTATGAGTGTGGGCACCTGCCGGCAGCCCCGGAGGCCCTGGCCTTAAGTGGC
CGTTTCTGGGCCTCGACAGTGCATGCCCTGGAGACTGACTCGCTGCCATGATCGTCAGC
ATCAAGGAGGGAGGCAGGACCAGGCCAGGTGGTCAGCCTGCCAACATGAGGGTGCAGAA
GTGCAGCTGTGCCTCGGATGGTGCCTCGTGCACAGGAGCTCCAGGCATAGGCGCTAGTG
TAGCCATCGAGGGACTTGACTTGTGTGTTCTGAAGTGTGAGGGTACCGAGAGCTG
GCGATGACTGAACTGCTGATGGACAAATGCTCTGTGCTCTAGTGAGCCCTGAATTGCTT
CCTCTGACAAGTTACCTCACCTAATTTGCTCTCAGGAATGAGAATCTTGGCCACTGGA
GAGCCCTTGCAGTTCTATTCTATTACTGCACTATATTCTAACGACTTACAT
GTGGAGATACTGTAACCTGAGGGCAGAAAGCCCANTGTGTCATTGTTACTTGTCTGTCAC
TGGATCTGGCTAAAGTCCACCACCTGGACCTAACGACCTGGGTTAAGTGTGGGT
TGTGCATCCCCAATCCAGATAATAAGACTTGTAAAACATGAATAAACACATTATTCT
AAAA

FIGURE 42

MQPLWLCWALWVLPLASPGAAALTGEQLLGSLRLQLKEVPTLDRADMEELVIPTHVRAQYV
ALLQRSHGDRSRGKRFQSFRREVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRLFQEP
VPKAALHRHGRLLSPRSARARVTVEWLVRDDGSNRTSLIDSRLVSHESGWKAFDVTEAVNF
WQQLSRPRQPLLLQSVQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTLDLGDYGAQ
GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCRQPPEALAFKWPF
LGPRQCIASETDSLPMIVSIKEGGRTQPQVVS LPNMRVQKCSCASDGALVPRRLQP

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 158-162

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 76-80

Casein kinase II phosphorylation site.

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

N-myristoylation site.

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

Amidation site.

amino acids 74-78

TGF-beta family signature.

amino acids 282-298

FIGURE 43

GTCTGTTCCCAGGAGTCCTCGGGCTGTTGTCAAGTGGCCTGATCGCGATGGGACAAA
GGCGCAAGTCGAGAGGAAACTGTTGTGCCTCTCATATTGGCGATCCTGTTGTGCTCCCTGG
CATTGGGCAGTGTACAGTGCACTCTCTGAACCTGAAGTCAGAATTCTGAGAATAATCCT
GTGAAGTTGTCCGTGCCTACTCGGGCTTTCTTCTCCCCGTGGAGTGGAAAGTTGACCA
AGGAGACACCACCAAGACTCGTTGCTATAATAACAAGATCACAGCTTCCTATGAGGACCGGG
TGACCTTCTTGCCAACCTGGTATCACCTCAAGTCCGTGACACGGGAAGACACTGGGACATAC
ACTTGATGGTCTCTGAGGAAGGCGGAAACAGCTATGGGAGGTCAAGGTCAAGCTCATCGT
GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCCTCCCTGCCACCATGGGAACCGGG
CAGTGCTGACATGCTCAGAACAAAGATGGTCCCCACCTCTGAATAACACCTGGTCAAAGAT
GGGATAGTGATGCCTACGAACAAAGATGGTCCCCACCTCTGAATAACACCTGGTCAAAGAT
GAATCCCACACAGGAGAGCTGGTCTTGATCCCCTGTCAGCCTCTGATACTGGAGAATACA
GCTGTGAGGCACCGAATGGTATGGACACCCATGACTTCAAATGCTGTGCGATGGAAGCT
GTGGAGCGGAATGTGGGGTCATCGTGGCAGCCGCTTGTAAACCTGATTCTCCTGGGAAT
CTTGGTTTTGGCATCTGGTTGCCTATAGCCGAGGCCACTTGACAGAACAAAGAAAGGA
CTTCGAGTAAGAAGGTGATTTACAGCCAGCCTAGTGGCCGAAGTGAAGGAGAATTCAAACAG
ACCTCGTCATTCCCTGGTGTGACCTGGTCGGCTACCGCCTATCATCTGCATTTGCCTTACT
CAGGTGCTACCGGACTCTGGCCCTGATGTCAGTTCACAGGATGCCTATTTGTCTTC
TACACCCCACAGGGCCCCCTACTTCTGGATGTGTTTAATAATGTCAGCTATGTGCC
ATCCTCCTCATGCCCTCCCTCCCTTACCACTGCTGAGTGGCCTGGAACCTGTTAAA
GTGTTATTCCCCATTCTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC
TTCTAAGTAGACAGCAAAATGGCGGGGTCGCAGGAATCTGCACTCAACTGCCACCTGGC
TGGCAGGGATCTTGAATAGGTATCTTGAGCTGGTCTGGCTCTTCTGTACTGAC
GACCAGGGCCAGCTGTTCTAGAGCGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGTTGG
TGATGACACTGGGTCTTCCATCTCTGGGGCCACTCTCTGTCTTCCATGGGAAGTG
CCACTGGATCCCTGCCCTGCTGAATACAAGCTGACTGACATTGACTGTCTGT
GGAAAATGGGAGCTTGTGGAGAGCATAGTAAATTTCAGAGAACTTGAAGCCAAAAG
GATTTAAAACCGCTGCTAAAGAAAAGAAAATGGAGGCTGGCGAGTGGCTACGCC
TAATCCCAGAGGCTGAGGCAGGCGGATCACCTGAGGTGGAGTTGGGATCAGCCTGACCA
ACATGGAGAAACCTACTGGAAATACAAGTTAGCCAGGCATGGTGGTGCATGCCTGTAGTC
CCAGCTGCTCAGGAGCCTGGCAACAAGAGCAAAACTCCAGCTCAAAAAAAA

FIGURE 44

MGTKAQVERKLLCLFILAIIICSLALGSVTVHSSEPEVRIENNPKLSCAYSGFSSPRVEW
KFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGYTCMVSEEGGNSYGEVKV
KLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIQMPTNPKSTRAFSNS
SYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVAAVLVTLI
LLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGFKQTSSFLV

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 238-255

N-glycosylation site.

amino acids 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 270-274

Casein kinase II phosphorylation site.

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,
193-197, 203-207, 287-291

N-myristoylation site.

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

FIGURE 45

CAGCGCGTGGCCGGCGCCGCTGTGGGACAGCATGAGCGCGGTTGGATGGCGCAGGTTGGA
GCGTGGCGAACAGGGCTCTGGGCCTGGCGCTGCTGCTGCTGCTCGGCCTCGGACTAGGCCT
GGAGGCCGCGCGAGCCGCTTCACCCGACCTCTGCCAGGCCAGGCCAGCTCAG
GCTCGTCCCACCAAGTCCAGTGCCGACCAGTGGCTATCGTGCCCCCACCTGG
CGCTGCGACAGGGACTTGGACTGCAGCGATGGCAGCGATGAGGAGGAGTCAGGATTGAGCC
ATGTACCCAGAAAGGCAATGCCACCGCCCCCTGGCCTCCCTGCCCTGCACCGCGTCA
GTGACTGCTGGGGAACTGACAAGAACTGCGCACTGCAGCCCTGGCCTGCCTAGCA
GGCGAGCTCCGTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGCTGCGACGGCCA
CCCAGACTGTCCCAGCTCCAGCGACGAGCTGGCTGTGGAACCAATGAGATCCTCCCGAAG
GGGATGCCACAACCATGGGCCCCCTGTGACCCCTGGAGAGTGTACCTCTCAGGAATGCC
ACAACCATGGGCCCCCTGTGACCCCTGGAGAGTGTCCCCTGTGGAAATGCCACATCCTC
CTCTGCCGGAGACCAGTCTGGAAGCCAACGCCTATGGGTTATTGCAGCTGCTGCCGTGC
TCAGTGCAAGCCTGGTCACGCCACCCCTCCCTTTGTCCCTGGCTCCGAGCCAGGAGCGC
CTCCGCCACTGGGTTACTGGTGGCATGAAGGAGTCCCTGCTGTCAGAACAGAAC
CTCGCTGCCTGAGGACAAGCACTTGCCACCACCGTCACTCAGCCCTGGCGTAGCCGGACA
GGAGGAGAGCAGTGTGGATGGTACCCGGCACACCAGCCCTCAGAGACCTGAGTTCTT
CTGGCCACGTGGAACCTCGAACCCGAGCTCCTGCAGAAGTGGCCCTGGAGATTGAGGGTCCC
TGGACACTCCCTATGGAGATCCGGGAGCTAGGATGGGAACCTGCCACAGCCAGAAC
GGGCTGGCCCCAGGCAGCTCCAGGGGTAGAACGCCCTGTGCTTAAGACACTCCCTGCTG
CCCCGTCTGAGGGTGGCGATTAAAGTTGCTTC

FIGURE 46

MSGGWMAQVGAWRTGALGLLLLLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCR
TSGLCVPLTWRCDRDLDSCDGSDEEEERICIEPCTQKGQC PPPGLPCPCTGVSDCSGGTDKKL
RNCSRRLACLAGELRCTLSDDCIPLTWRCDGHPDCPDSSDELCGTNEILPEGDATTMGPPVT
LESVTSLRNATTMGPPTLESVPSVGNATSSAGDQSGSPTAYGVIAAAAVLSASLVTATLL
LLSWLRAQERLRPLGLLVAMKESLLLSEQKTSLP

Signal sequence:

amino acids 1-30

Transmembrane domain:

amino acids 230-246

N-glycosylation site.

amino acids 126-130, 195-199, 213-217

Casein kinase II phosphorylation site.

amino acids 84-88, 140-144, 161-165, 218-222

N-myristoylation site.

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,
224-230, 230-236, 263-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 44-55

Leucine zipper pattern.

amino acids 17-39

FIGURE 47

CCCACGCGTCCGGTCTCGCTCGCTCGCGCAGCGGCCAGCAGAGGTGCGCACAGATGCGG
GTTAGACTGGCGGGGGAGGAGGCAGGAGGAAGGAAGCTGCATGCATGAGACCCACAGA
CTCTTGCAAGCTGGATGCCCTGTGGATGAAAGATGTTATCATGGAATGAACCCGAGCAATG
GAGATGGATTCTAGAGCAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTG
GCCGTGATCCTGTGGTTCAGCTGGCGCTGTGCTTCGGCCCTGCACAGCTCACGGCGGGTT
CGATGACCTTCAAGTGTGCTGACCCGGCATTCCGAGAAATGGCTTCAGGACCCCCAGCG
GAGGGGTTTCTTGAGGCTCTGTAGCCGATTCACTGCCAAGACGGATTCAAGCTGAAG
GGCGCTACAAAGAGACTGTGTTGAAGCATTAAATGAAACCTAGGCTGGATCCAAGTGA
TAATTCCATCTGTGCAAGAACGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTCA
ACAAGACATATAGACATGGAGAGAACGCTAACATCACTTGTCACTGAAGGATTCAAGATCCGG
TACCCGACCTACACAATATGGTTTATTATGTCGCGATGGAACGTGGAATAATCTGCC
CATCTGTCAAGGCTGCCTGAGACCTCTAGCCTCTTAATGGCTATGTAAACATCTCTGAGC
TCCAGACCTCCTCCGGTGGGACTGTGATCTCCTATCGCTGCTTCCGGATTAAACTT
GATGGGTCTGCGTATCTTGAGTGCTTACAAAACCTTATCTGGTCGTCCAGCCCACCCGGTG
CCTTGCTCTGGAAGCCCAAGTCTGTCCACTACCTCCAATGGTAGTCACGGAGATTCGTCT
GCCACCCGGCCCTGTGAGCGCTACAACCACGGAACGTGGTGGAGTTACTGCGATCCT
GGCTACAGCCTCACCAAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTCTTC
TTATCAAGTCTACTGCATCAAATCAGAGCAAACGTGGCCAGCACCCATGAGACCCCTCTGA
CCACGTGGAAGATTGTGGCGTTACGGCAACCAGTGTGCTGCTGGTGTGCTCGTCATC
CTGGCCAGGATGTTCCAGACCAAGTTCAAGGCCACTTCCCCCAGGGGGCTCCCCGGAG
TTCCAGCAGTGACCCCTGACTTGTGGTAGACGGCGTGGCTCATGCTCCGTCTATG
ACGAAGCTGTGAGTGGCGCTTGAGTGCTTAGGCCCGGGTACATGGCCTCTGTGGGCCAG
GGCTGCCCTTACCGTGGACGACCAGAGCCCCCAGCATACCCGGCTCAGGGACACGGA
CACAGGCCAGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTTTGAGCTGCTCCAAA
GTCTGTATTCACCTCCAGGTGCCAAGAGAGCACCCACCCCTGCTCGGACAACCTGACATA
ATTGCCAGCAGGCAGAGGAGGTGGCATCCACCAGGCCAGGCATCCATCATGCCACTGGGT
GTTGTTCTAAGAAACTGATTGATTAAAAAATTCCCAAAGTGTCTGAAGTGTCTTTCAA
ATACATGTTGATCTGTGGAGTTGATTCTTCTCTTGTTTAGACAAATGTAAACAA
AGCTCTGATCCTTAAAATTGCTATGCTGATAGAGTGGTAGGGCTGGAAGCTGATCAAGTC
CTGTTCTTCTTGACACAGACTGATTAAAATTAAAAGNAAAAAA

FIGURE 48

MYHGMNPSNGDGFLEQQQQQQQQPQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI
PENGFRTPSGGVFFEGSVARFHQCQDGFKLKKGATKRLCLKHFNGTLGWIPSDNSICVQEDCRI
PQIEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPLICQGCLRPLAS
SNGYVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSPRCLALEAQVCPLP
PMVSHGDFVCHPRPCERYNHGTVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQT
WPSTHETLLTTWKIVAFATSVLLVLLVILARMQTKFAHFPPRGPPRSSSDPDFVVVD
GVPVMLPSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGDTDTGPGESETCDS
VSGSSELLQSLYSPPRCQESTHPASDNPDIIASTAEEVASTSPGIHHAHWVLFLRN

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 325-344

N-glycosylation site.

amino acids 104-108, 134-138, 192-196

Casein kinase II phosphorylation site.

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,
364-368, 380-384, 467-471, 468-472

N-myristoylation site.

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,
478-484

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 394-405

FIGURE 49

CCACCGCGTCCGCTCCCGCCCTCCCCCCCCTGGCTCGGGTCCGTGGCTAGAGA
TGCTGCTGCCCGGGTGCAGTTGTCGCGCACGCCCTGCCCGCAGCCGCTCCACGCCGT
AGCGCCCGAGTGTGGGGGGCGCACCCGAGTCGGGCCATGAGGCCGGAACCGCGCTACAGG
CCGTGCTGCTGGCCGTGCTGGTGGGCTGCAGGGCGACGGGCGCTGCTGAGTGCC
TCGGATTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGAGGGACACAGAGGCCTGTTA
TAAAGTCATTACTTCATGATACTTCTCGAAGACTGAACCTTGAGGAAGCCAAGAAGCCT
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAAACTGATAGAA
AAGTCATTGAAAACCTTGCATCTGATGGTACTTCTGGATTGGCTCAGGAGGCCTGA
GGAGAAACAAAGCAATAGCACAGCCTGCCAGGACCTTATGCTGGACTGATGGCAGCATAT
CACAATTTAGGAACGGTATGTGGATGAGCCGTGCAGCAGGGCTGCGTGGTCATG
TACCATCAGCCATGGCACCCGCTGGCATCGGAGGCCCTACATGTTCCAGTGGAAATGATGA
CCGGTGCAACATGAAGAACAAATTCAATTGCAAATATTCTGATGAGAACACCAGCAGTCCTT
CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAAGAACACAG
GAAGAAGATGCCAAAAAAACATTAAAGAAAGTAGAGAACAGCTGCCTGAATCTGGCTACAT
CCTAATCCCCAGCATTCCCTCTCCTCCTGGTCACCACAGTTGTATGTTGGTTT
GGATCTGTAGAAAAAGAAAACGGGAGCAGCCAGACCCCTAGCACAAAGAACACACCATC
TGGCCCTCTCCTCACCAAGGGAAACAGCCGGACCTAGAGGTCTACAATGTCATAAGAAAACA
AAGCGAAGCTGACTTAGCTGAGACCCGCCAGACCTGAAGAATATTCAATTCCGAGTGTGTT
CGGGAGAACCCACTCCGATGACATGTCTGTGACTATGACAACATGGCTGTGAACCCATCA
GAAAGTGGTTGTGACTCTGGTGGAGAGTGGATTGTGACCAATGACATTATGA
GTTCTCCCCAGACCAATGGGAGGAGTAAGGAGTCTGGATGGTGAAATGAAATATATG
GTTATTAGGACATATAAAACTGAAACTGACAACAATGGAAAAGAAATGATAAGCAAATC
CTCTTATTTCTATAAGGAAAATACACAGAACGGTCTATGAACAAGCCTAGATCAGGTCTGT
GGATGAGCATGTGGTCCCCACGACCTCTGGACCCCCACGTTGGCTGTATCCTTTAT
CCCAGCCAGTCATCCAGCTGACCTTATGAGAACGGTACCTGCCAGGTCTGGCACATAGTA
GAGTCTCAATAATGTCACTTGGTTGGTGTATCTAACCTTAAGGGACAGAGCTTACCTG
GCAGTGATAAAAGATGGCTGTGGAGCTGGAAAACCACCTCTGTTCTGCTATACAG
CAGCACATATTATCATAACAGAACAGAAAATCCAGAACATCTTCAAAGCCCACATATGGTAGCACAG
GTTGGCCTGTGCATCGCAATTCTCATATCTGTTTTCAAAGAACATAAAATCAAATAAGA
GCAGGAAAAAA

FIGURE 50

MRPGTALQAVILLAVLLVGLRAATGRLLSASDLRGGQPVCRGGTQRPCYKVIYFHDTSRRL
NFEEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDL
YAWTDGSISQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNFICKY
SDEKPAVPSREAEGEETELTPVLPEETQEEDAKKTFKESREAALNAYILIPSIPLLL
VTTVVCWVWICRKRKREQPDPSCKQHTIWPSPHQGNSPDLEVYNVIRKQSEADLAETRPDL
KNISFRVCSGEATPDDMSCDYDNMAVNPSSEGFTLVSVESGFVTNDIYEFSPDQMGRSKES
GWVENEIYGY

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 117-121, 312-316

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 296-300

Casein kinase II phosphorylation site.

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,
299-303, 306-310, 323-327

N-myristoylation site.

amino acids 18-24, 37-43, 76-82, 146-152

FIGURE 51

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTGCTGAAGGGCTGGATGTACGC
ATCCGCAGGTTCCCGCGGACTTGGGGCGCCGCTGAGCCCCGGCGCCGCAGAAGACTTGT
GTTGCCTCCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCCTACCACCATGATCACTGGTGT
GTTCAGCATGCGCTTGTGGACCCCAGTGGCGTCCTGACCTCGCTGGCGTACTGCCTGCACC
AGCGCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCATGCCAGTGTCCGGTCACCGCAGC
CTGCTGAAGTTGAAAATGGTGCAGGTGTTGACACGGGGCTGGAGTCCCTCTCAAGCC
GCTCCGCTGGAGGAGCAGGTAGAGTGGAACCCCCAGCTATTAGAGGTCCCACCCAACTC
AGTTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATAATTCTCCTTACGACTCT
CAATACCATGAGACCACCCCTGAAGGGGGCATGTTGCTGGCAGCTGACCAAGGTGGCAT
GCAGCAAATGTTGCCTTGGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCCTTC
TTTCACCAACCTCAACCCACAGGAGGTCTTATTGTTCCACTAACATTTCGGAATCTG
GAGTCCACCCGTTGTTGCTGGCTGGCTTTCCAGTGTAGAAAGAAGGACCCATCATCAT
CCACACTGATGAAGCAGATTAGAAGTCTTGTATCCAACCTACCAAGCTGCTGGAGCCTGA
GGCAGAGAACCAAGAGGCCGGAGGCAGACTGCCTCTTACAGCCAGGAATCTCAGAGGATTG
AAAAAGGTGAAGGACAGGATGGCATTGACAGTAGTGATAAAAGTGGACTTCTCATCCTCCT
GGACAACGTGGCTGCCGAGCAGGCACACAACCTCCAAGCTGCCCCATGCTGAAGAGATTG
CACGGATGATCGAACAGAGAGCTGGACACATCCTGTACATACTGCCAAGGAAGACAGG
GAAAGTCTCAGATGGCAGTAGGCCATTCCACATCCTAGAGAGCAACCTGCTGAAAGC
CATGGACTCTGCCACTGCCCCGACAAGATCAGAAAGCTGTATCTATGCGGCTATGATG
TGACCTTCATACCGCTTAATGACCCCTGGGATTTGACCAAAATGCCACCGTTGCT
GTTGACCTGACCATGGAACCTTACCAAGCACCTGGAATCTAAGGAGTGGTTGTGCAGCTCTA
TTACCAAGGGAAAGGAGCAGGTGCCAGAGGGTTGCCCTGATGGCTCTGCCGCTGGACATGT
TCTTGAATGCCATGTCAGTTATACCTTAAGCCCAGAAAATACCATGCACTCTGCTCTCAA
ACTCAGGTGATGGAAGTTGGAAATGAAGAGTAACTGATTATAAAAGCAGGATGTGTTGATT
TTAAAATAAAGTGCCTTATACAATG

FIGURE 52

MITGVFSMRLWTPVGVLTSLAYCLHQRRVALAELQEADGQCPVDRSLLKLKMVQVVFRHGAR
SPLKPLPLEEQVEWNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQL
TKVGMQQMFALGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLQLFQCQKE
GPIIIHTDEADSEVLYPNYQSCWSLRQRTRGRRTASLQPGISEDLKKVKDRMGIDSSDKVD
FFILLDNVAEQAHNLSCPMLKRFARMIEQRAVDTSLYILPKEDRESLQMAVGPFLHILES
NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPPFAVDLTMELYQHLESKEW
FVQLYYHGKEQVPRGCPDGLCPLDMFLNAMSVTLSPEKYHALCSQTQVMEVGNEE

Signal sequence:

amino acids 1-23

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 218-222

Casein kinase II phosphorylation site.

amino acids 87-91, 104-108, 320-324

Tyrosine kinase phosphorylation site.

amino acids 280-288

N-myristoylation site.

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

Amidation site.

amino acids 216-220

Leucine zipper pattern.

amino acids 10-32

Histidine acid phosphatases phosphohistidine signature.

amino acids 50-65

FIGURE 53

CTCCTCTAACATACTTGCAGCTAAAACATAATGCTGCTGGGACCTCCTCTAGCCT
TAAATTTCAGCTCATCACCTCACCTGCCTGGTCATGGCTCTGCTATTCTCCTTGATCCTT
GCCATTGCACCAGACCTGGATTCCCTAGCGTCTCCATCTGGAGTGCAGCTGGTGGGGCCT
CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGGCACCGTGTGATG
ACGGCTGGACATTAAGGACGTGGCTGTGTTGCCGGAGCTGGCTGTGGAGCTGCCAGC
GGAACCCCTAGTGGTATTTGTATGAGCCACCAGCAGAAAAAGAGCAAAGGTCTCATCCA
ATCAGTCAGTTGCACAGGAACAGAAGATACTGGCTCAGTGTGAGCAAGAAGAAGTTATG
ATTGTTCACATGATGAAGATGCTGGGCATCGTGTGAGAACCCAGAGAGCTCTTCTCCCCA
GTCCCAGAGGGTGTCAAGGCTGGCTGACGCCCTGGCATTGCAAGGGACGCGTGGAAAGTGAA
GCACCAGAACCAAGTGGTATACCGTGTGCCAGACAGGCTGGAGCCTCCGGCCGCAAAGGTGG
TGTGCCGGCAGCTGGATGTGGAGGGCTGTACTGACTCAAAAACGCTGCAACAAGCATGCC
TATGGCCAAAACCCATCTGGCTGAGCCAGATGTCATGCTCAGGACGAGAAGCAACCCTCA
GGATTGCCCTCTGGCCTTGGGAGAACACACCTGCAACCAGATGAAGACACGTGGTCG
AATGTGAAGATCCCTTGACTTGAGACTAGTAGGAGGAGACAACCTCTGCTCTGGCGACTG
GAGGTGCTGACAAGGGCTATGGGCTCTGTCTGTGATGACAACACTGGGAGAAAAGGAGGA
CCAGGTGGTATGCAAGCAACTGGCTGTGGGAAGTCCCTCTCCCTCCTCAGAGACCGGA
AATGCTATGCCCTGGGTTGCCGCATCTGGCTGGATAATGTTGCTCAGGGAGGGAG
CAGTCCCTGGAGCAGTGCAGCACAGATTTGGGGTTTCACGACTGCACCCACCAGGAAGA
TGTGGCTGTCATGCTCAGTGTAGGTGGCCATCATCTAATCTGTTGAGTGCCTGAATAGAA
AAAAACACAGAAGAAGGGAGCATTACTGTCTACATGACTGCATGGGATGAACACTGATCT
TCTTCTGCCCTGGACTGGACTTATACTTGGTCCCCCTGATTCTCAGGCCTTCAGAGTTGG
ATCAGAACTTACAACATCAGGTCTAGTTCTCAGGCCATCAGACATAGTTGGAACATACATCA
CCACCTTCCTATGTCTCCACATTGCACACAGCAGATTCCAGCCTCCATAATTGTGTGTAT
CAACTACTTAAATAACATTCTCACACACACACACACACACACACACACACACACACATA
CACCAATTGTCCTGTTCTCTGAAGAACTCTGACAAAATACAGATTTGGTACTGAAAGAGA
TTCTAGAGGAACGGAATTAAAGGATAAATTCTGTAATTGGTTATGGGTTCTGAAATTG
GCTCTATAATCTAATTAGATATAAAATTCTGGTAACCTTATTACAATAATAAGATAGCAC
TATGTGTTCAAA

FIGURE 54

MALLFSLILAICTRPGLASPSGVRLVGGLHRCEGRVEVEQKGQWGTVCDDGWDIKDVAVLC
RELGCAGAASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEEVYDCSHDEDAGASC
ENPESSFSPVPEGVRLADGPGHCKGRVEVKHQNQWYTVCQTGWSLRAAKVVCRQLGCGRAVL
TQKRCNKHAYGRKPIWLSQLMCSGREATLQDCPSGPWGKNTCNHDEDTWVECEDPFDLRLVG
GDNLCSGRLEVLHKGVWGSVCDDNWGEKEDQVVCKQLGCGKSLSPSFRDRKCYGPGVGRIWL
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

Signal sequence:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,
267-271, 294-298, 316-320, 336-340

N-myristoylation site.

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,
180-186, 263-269, 286-292

Amidation site.

amino acids 196-200

Speract receptor repeated domain signature.

amino acids 29-67, 249-287

FIGURE 55

ACTGCACTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGAC
CCACCGCGTCCCGGGACCGGTGGCGGACCGTGCGGCCGGCTACCAGGAAGAGTCTGCCGAAG
GTGAAGGCCATGGACTTCATCACCTCCACAGCCATCCTGCCCTGCTGTTGGCTGCCTGG
CGTCTTCGGCCTCTTCCGGCTGCTGCAGTGGTGCGCGGGAAAGGCCTACCTGCGGAATGCTG
TGGTGGTGTACAGGGGCCACCTCAGGGCTGGCAAAGAATGTGAAAAGTCTTCTATGCT
GCGGGTGTAAACTGGTGCTCTGTGGCCGAATGGTGGGGCCCTAGAAGAGCTCATCAGAGA
ACTTACCGCTTCTCATGCCACCAAGGTGCAGACACACAAGCCTACTTGGTGACCTTCGACC
TCACAGACTCTGGGCCATAGTTGCAGCAGCAGCTGAGATCCTGCAGTGCCTTGGCTATGTC
GACATACTTGTCAACAATGCTGGATCAGCTACCGTGGTACCATCATGGACACACCAGTGG
TGTGGACAAGAGGGTCATGGAGACAAACTACTTGGCCAGTTGCTCTAACGAAAGCACTCC
TGCCCTCCATGATCAAGAGGAGGCAAGGCCACATTGTCGCCATCAGCAGCATCCAGGGCAAG
ATGAGCATTCTTTGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTCTTGA
CTGTCGTGCCAGAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA
TCCACACCAACCTCTGTAAATGCCATACCGCGGATGGATCTAGGTATGGAGTTATGGAC
ACCACCAACAGCCCAGGGCGAAGCCCTGTGGAGGTGGCCAGGATGTTCTGCTGCTGG
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTACTGCCTCCTGGCTGTTATCTCGAA
CTCTGGCTCCTGGCTCTTCTTCAGCCTCATGGCCTCCAGGGCCAGAAAAGAGCGGAAATCC
AAGAACTCCTAGTACTCTGACCAGCCAGGGCAGGGCAGAGAAGCAGCACTCTAGGCTTGC
TTACTCTACAAGGGACAGTTGCATTTGAGACTTTAATGGAGATTGTCTACAAGTGG
AAAGACTGAAGAAACACATCTCGTGCAGATCTGCTGGCAGAGGACAATAAAAACGACAACA
AGCTTCTTCCCAGGGTGAGGGAAACACTTAAGGAATAATGGAGCTGGGTTAACACT
AAAAACTAGAAATAAACATCTCAAACAGTAAAAAAAAAAAAAGGGCGGCCGACTCTAG
AGTCGACCTGCAGAAGCTTGGCCGCATGGCCAACTTGTTATTGCAGCTTATAATGGTTAC

FIGURE 56

MDFITSTAILPLLFGCLGVFGLFRLLQWVRGKAYLRNAVVVITGATSGLGKEAKVFYAAAGA
KLVLCGRRNGGALEELIRELTASHATKVQTHKPYLVTFDLTDGAI
VAAAEEILQCFGYVDIL
VNNAGISYRGTIMDTVDVKRVMETNYFGPVALTKALLPSMIKRRQGHIVAISSIQGKMSI
PFRSAYAASKHATQAFFDCLRAEMEQYEIEVTVISPGYIHTNLSVN
AITADGSRYGVMDTTT
AQGRSPVEVAQDVLA AVGKKKDVLADLLPSLAVYLRTLAPGLFFSLMASRARKERKSNS

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 104-120, 278-292

N-glycosylation site.

amino acids 228-232

Glycosaminoglycan attachment site.

amino acids 47-51

Casein kinase II phosphorylation site.

amino acids 135-139, 139-143, 253-257

Tyrosine kinase phosphorylation site.

amino acids 145-153, 146-153

N-myristoylation site.

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

Amidation site.

amino acids 265-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 6-17

FIGURE 57

CCACCGCGTCCGCTGGTGTAGATCGAGCAACCCCTAAAGCAGTTAGAGTGGTAAAAAA
AAAAAAAAACACACCAAACGCTCGCAGCCACAAAAGGGATGAAATTCTTCTGGACATCCTC
CTGCTTCTCCCGTTACTGATCGTCTGCTCCCTAGAGTCCTCGTGAAGCTTTTATTCTAA
GAGGAGAAAATCAGTCACCGGCAGAACATCGTGTGATTACAGGAGCTGGCATGGAATTGGGA
GAUTGACTGCCTATGAATTGCTAAACTAAAGCAAGCTGGTCTCTGGATATAAATAAG
CATGGACTGGAGGAAACAGCTGCCAAATGCAAGGGACTGGGTGCCAAGGTTCATACCTTGT
GGTAGACTGCAGCAACCGAGAAGATATTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG
GAGATGTTAGTATTAGTAAATAATGCTGGTAGTCTATACATCAGATTGTTGCTACA
CAAGATCCTCAGATTGAAAAGACTTTGAAGTTAATGTACTTGACATTTCTGGACTACAAA
GGCATTCTCCTGCAATGACGAAGAATAACCATGGCCATTGTCACTGTGGCTCGGCAG
CTGGACATGTCGGTCCCCTTACTGGCTTACTGTTCAAGCAAGTTGCTGTTGGA
TTTCATAAAACTTGACAGATGAACGGCTGCCTACAAATACTGGAGTCAAAACAACATG
TCTGTCCTAATTGTAACACTGGCTCATCAAAATCCAAGTACAAGTTGGACCCA
CTCTGGAACCTGAGGAAGTGGTAAACAGGGCTGATGCATGGGATTCTGACTGAGCAGAAGATG
ATTTTATTCCATCTCTATAGCTTTAACACATTGAAAGGATCCTCCTGAGCGTT
CCTGGCAGTTTAAAAGAAAATCAGTGTAAAGTTGATGCAGTTATTGGATATAAATGA
AAGCGCAAAGCACCTAGTTCTGAAAACGTGATTACCAAGGTTAGGTTGATGTCATCTA
ATAGGCCAGAATTAAATGTTGAACCTCTGTTTTCTAATTATCCCCATTCTCAATA
TCATTGGAGGCTTGGCAGTCTCATTACTACCACCTGTTCTTAGCCAAAGCTGATT
ACATATGATATAAACAGAGAAATACCTTAGAGGTGACTTTAAGGAAAATGAAGAAAAGAA
CCAAAATGACTTATTAAAATAATTCCAAGATTATTGTGGCTCACCTGAAGGCTTGCAA
AATTGTACCATAACCGTTATTAAACATATATTATTATTGATTGACTTAAATTGT
ATAATTGTGTTCTTTCTGTTCTACATAAAATCAGAAACTTCAAGCTCTAAATAAAA
TGAAGGACTATATCTAGGGTATTTCACAATGAATATCATGAACCTCAATGGTAGGTTTC
ATCCTACCCATTGCCACTCTGTTCTGAGAGATACCTCACATTCCAATGCCAACATTCT
GCACAGGGAGCTAGAGGTGGATACACGTGTTGCAAGTATAAAAGCATCACTGGATTAAAG
GAGAATTGAGAGAATGTACCCACAAATGGCAGCAATAATAATGGATCACACTTAAAAAAA
AAAAAAA
AAAAAAA

FIGURE 58

MKFLLDILLPLLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK
LVLWDINKHGLEETAACKCKGLGAKVHTFVVDCSNREDIYSSAKVKAEIGDVSILVNNAGVV
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLLAYC
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVVNRLMH
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMKAQ

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34, 283-287

Casein kinase II phosphorylation site.

amino acids 52-56, 95-99, 198-202, 267-271

N-myristoylation site.

amino acids 43-49, 72-78, 122-128, 210-216

FIGURE 59

CCCCACCGCGTCCGGGAGCGCGTGGGTCGACTAGTTCTAGATCGCGAGCGGCCGCCGCGCTC
AGGGAGGAGCACCGACTCGCGCCGACCCCTGAGAGATGGTGGCATGTGGAAGGTTGATTG
TTTCGCTGGTCCTGTTGATGCCTGGCCCCCTGTGATGGGCTGTTCTGCTCCCTATAAGAAAGT
GTTTCCATGCCACCTAACGGAGACTCAGGACAGCATTATTCTCACCCCTAACATTGAAGC
TGGGAAGATCCAAAAAGGAAGAGAATTGAGTTGGTCGGCCCTTCCCAGGACTGAACATGA
AGAGTTATGCCGGCTTCCCTCACCGTGAATAAGACTTACAACAGCAACCTCTTCTGGTTC
TTCCCAGCTCAGATAACGCCAGAACAGATGCCAGTAGTTCTGGCTACAGGGTGGGCCGGG
AGGTTCATCCATGTTGGACTCTTGGAACATGGGCTTATGTTGTCACAAGTAACATGA
CCTTGGGTGACAGAGACTCCCTGGACCACAACGCTCTCCATGCTTACATTGACAATCCA
GTGGGCACAGGCTTCAGTTACTGATGATAACCCACGGATATGCAGTCATGAGGACGATGT
AGCACGGGATTATACAGTGCACAAATTCAAGTTCCAGATATTCTGAAATATAAAAATA
ATGACTTTATGTCACTGGGGAGTCTTATGCAGGGAAATATGTGCCAGCCATTGCACACCTC
ATCCATTCCCTCAACCCGTGAGAGAGGTGAAGATCAACCTGAACGGAATTGTATTGGAGA
TGGATATTCTGATCCGAATCAATTATAGGGGCTATGCAAGAATTCTGTAACCAAATTGGCT
TGGTGGATGAGAAGCAAAAAAGTACTTCCAGAAGCAGTGCATGAATGCATAGAACACATC
AGGAAGCAGAACTGGTTGAGGCCTTGAAATACTGGATAAACTACTAGATGGCAGCTAAC
AAGTGATCCTCTTACTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTGCCTG
GCACGGAACCTGAGGATCAGCTTACTATGTGAAATTGTCACTCCAGAGGTGAGACAA
GCCATCCACGTGGGAATCAGACTTTAATGATGGAACTATAGTTGAAAGTACTGCGAGA
AGATAACAGTACAGTCAGTTAACGGCATGGTTAACTGAAATCATGAATAATTATAAGGTTCTGA
TCTACAATGGCCAAC TG GACATCATCGTGGCAGCTGCCCTGACAGAGCGCTCTTGATGGGC
ATGGACTGGAAAGGATCCAGGAATACAAGAAGGAGAAAAAAAGTTGGAAGATCTTAA
ATCTGACAGTGAAGTGGCTGGTTACATCCGGCAAGGGGTGACTTCCATCAGTAATTATC
GAGGTGGAGGACATATTACCCATGACCAGCCTTGAGAGCTTGACATGATTAATCGA
TTCATTATGGAAAAGGATGGGATCCTTATGTTGGAAAACTACCTCCAAAAGAGAACAT
CAGAGGTTTCATTGCTGAAAAGAAAATCGTAAAAACAGAAAATGTGATAGGAATAAAAAAA
TTATCTTTCATATCTGCAAGATTTTCTCATCAATAAAATTATCCTGAAACAAGTGAGC
TTTGTGTTGGGGAGATGTTACTACAAAATTAAACATGAGTACATGAGTAAGAATTACA
TTATTTAACTAAAGGATGAAAGGTATGGATGATGTGACACTGAGACAAGATGTATAATGA
AATTTAGGGTCTTGAATAGGAAGTTAATTCTCTAACAGTAAGTGAAGTGAAGCTTG
TAACAAACAAAGCTGTAACATCTTCTGCCAATAACAGAACAGTTGGCATGCCGTGAAGGT
GTTTGGAAATATTATTGGATAAGAATAGCTCAATTATCCAAATAATGGATGAAGCTATAA
TAGTTTGGGAAAAGATTCTCAAATGTATAAAGTCTTAGAACAAAAGAATTCTTGAAATA
AAAATATTATAATAAAAGTAAAAAAAAAA

FIGURE 60

MVGAMWKVIVSLVLLMPGCDGLFRSLYRSVSMPPKGDSGQPLFLTPYIEAGKIQKGREL
VGPFPGNLNMKSYAGFLTVDKTYNSNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH
GPYVVTSNMTLDRDFPWTTTLSMLYIDNPVGTGFSFTDDTHGYAVNEEDDVARDLYSALIQF
FQIFPEYKNNDFYVTGESYAGKYVPAIAHLIHSLNPVREVKINLNGIAIGDGYSDPESIIGG
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEEAFEILDKLLGDLTSDPSYFQNVTG
CSNYYNFLRCTEPEDQLYYVKFLSLPEVRQAIHVGNTFNDGTIVEKYLREDTVQSVKPWLT
EIMNNYKVLIYNGQLDIIVAAAALTERSLMGMDWKGSQEYKKAEKVWKIFKSDSEVAGYIRQ
AGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYKGWDPYVG

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 81-85, 132-136, 307-311, 346-350

Casein kinase II phosphorylation site.

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,
353-357, 424-428

Tyrosine kinase phosphorylation site.

amino acids 423-432

N-myristoylation site.

amino acids 22-28, 110-116, 156-162, 232-238

Serine carboxypeptidases, serine active site.

amino acids 200-208

Crystallins beta and gamma 'Greek key' motif signature.

amino acids 375-391

FIGURE 61

CGAGGGCTTTCGGCTCCGAATGGCACATGTGGAATCCCAGTCCTGTTGGCTACAACAT
TTTCCCTTCTAACAGTCTAACAGCTGTTAACAGCTAGTGATCAGGGGTTCTTCTT
GCTGGAGAAGAAAGGGCTGAGGGCAGAGCAGGGCACTCTCACTCAGGGTGACCAGCTCCTTG
CCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCGGAGTGAGGTGATGGAAG
TCTAAAATAGGAAGGAATTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC
CTGGGGAGGGCCTGCCTAACAGCTTCAAAAAACAGGAGCGACTTCCACTGGCTGGGAT
AAGACGTGCCGTAGGATAGGGAAAGACTGGGTTAGTCCTAACATATCAAATTGACTGGCTGGG
TGAACCTCAACAGCCTTTAACCTCTGGAGATGAAAACGATGGCTTAAGGGGCCAGAAA
TAGAGATGCTTGTAAAATAAAATTAAAGCAAGTATTTATAGCATAAAGGCTAGA
GACCAAAATAGATAACAGGATTCCCTAACATTCTAACAGAGGGAGAAAGTATGTTAAAATA
GAAAAACCAAAATGCAGAAGGAGGAGACTCACAGAGCTAACACCAGGATGGGACCTGGTC
AGGCCAGCCTTTGCTCCTCCGGAAATTATTTGGTCTGACCACTCTGCCCTGTGTTT
GCAGAACATCATGTGAGGGCCAACCGGGGAAGGTGGAGCAGATGAGCACACACAGGAGCCGTCT
CCTCACCGCCGCCCTCTCAGCATGGAACAGAGGCAGCCCTGGCCCCGGGCCCTGGAGGTGG
ACAGCCGCTCTGGTCTGCTCAGTGGCTGGGTGCTGCTGGCCCCCCCAGCAGCCGGC
ATGCCTCAGTCAGCACCTCCACTCTGAGAACATCGTACTGGACCTAACCAACTTGACCGT
CCACCAAGGGACGGGGCCGTCTATGTGGGGCCATCAACCGGGTCTATAAGCTGACAGGCA
ACCTGACCATCCAGGTGGCTCATAACAGACAGGGCAGAAGAGGACAACAAGTCTCGTTACCCG
CCCCTCATCGTCAGCCCTGCAGCGAAGTGTCAACCCCTACCAACAATGTCAACAAAGCTGCT
CATCATTGACTACTCTGAGAACCGCCTGCTGGCCTGTGGAGCCTTACCAAGGGGCTGCA
AGCTGCTGCGGCTGGATGACCTCTTCATCCTGGTGGAGCCATCCCACAAGAAGGAGCACTAC
CTGTCCAGTGTCAACAAGACGGGACCATGTACGGGTGATTGTGCGCTCTGAGGGTGAGGA
TGGCAAGCTCTCATCGGCACGGCTGTGGATGGAAGCAGGATTACTTCCGACCCCTGTCCA
GCCGGAAGCTGCCCGAGACCCCTGAGTCCTCAGCCATGCTGACTATGAGCTACACAGCGAT
TTTGTCTCCTCTCATCAAGATCCCTCAGACACCCCTGCCCTGGTCTCCACTTTGACAT
CTTCTACATCTACGGCTTGCTAGGGGCTTGTCTACTTCTACTGTCCAGCCGAGA
CCCCTGAGGGTGTGGCCATCAACTCCGCTGGAGACCTCTTACACCTCACGCATCGCG
CTCTGCAAGGATGACCCCAAGTCCACTCATACGTGCTCCCTGCCCTGGCTGCACCCGGC
CGGGTGGAAATACCGCCTCGCAGGCTGCTTACCTGGCCAAGCCTGGGACTCACTGGCCC
AGGCCTTCAATATCACAGCAGGACGATGTACTCTTGCATCTTCCAAAGGGCAGAAG
CACTATCACCCGGCCGATGACTCTGCCCTGTGTGCCTTCCCTATCCGGCCATCAACTT
GCAGATCAAGGAGCGCTGCAGTCCTGCTACCAGGGCAGGGCACCTGGAGCTCAACTGGC
TGCTGGGAAGGACGTCAGTGCACGAAGGCGCTGCCCCATCGATGATAACTCTGTGGA
CTGGACATCAACCAGCCCTGGGAGGCTCAACTCCAGTGGAGGGCTGACCCCTGTACACCAC
CAGCAGGGACCGCATGACCTCTGTGGCCTCTACGTTACAACGGCTACAGCGTGGTTTG
TGGGACTAAGAGTGGCAAGCTGAAAAAGTAAGAGTCTATGAGTCAGATGCTCAATGCC
ATTCACCTCCTCAGCAAAGAGTCCCTCTGGAGGTAGCTATTGGTGGAGATTAACTATAG
GCAACTTATTCTGGGAACAAAGGTGAATGGGAGGTAAAGAAGGGGTTAATTGTG
ACTTAGCTTAGCTACTCCCTCAGCCATCAGTCATTGGTATGTAAGGAATGCAAGCGTA
TTCAATATTCCAAACTTAAGAAAAACTTAAAGAAGGTACATCTGCAAAAGCAAA

FIGURE 62

MGTLGQASLFAPPGNYFWSDHSALCFAESCEGQPGKVEQMSTHRSRLLTAAPLSMEQRQPWP
RALEVDSRSVVLSSVVWLLAPPAAGMPQFSTFHSENRDWTNFNHLTVQGTGAVYVGAINRV
YKLGNLTIQVAHKTGPEEDNKSRYPPLIVQPCSEVLTLTNNVNKLLIIDYSENRLLAGSL
YQGVCKLLRLDDLFLILVEPSHKKEHYLSSVNKTGTMYGVIVRSEGEGDKLFIGTAVDGKQDY
FPTLSSRKLP RDPESSAMLDYELHSDFVSSLIKIPSDTLALVSHFDIFYIYGFASGGFVYFL
TVQPETPEGVAINSAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRGVEYRLLQAAYLAKP
GDSLAQAFNITSQDDVLFAIFSKGQKQYHHPPDDSA LCAFPIRAINLQIKERLQSCYQGEGN
LELNWLLGKD VQCTKAPVPIDDNFCGLDINQPLGGSTPV EGLTLYTTSRDRMTSVASYVYNG
YSVVFVGTKSGKLKKV RVYEFRCSNAIHLLSKE SLLLEG SYWWRFNYRQLYFLGEQR

Signal sequence:

amino acids 1-32

Transmembrane domain:

amino acids 71-87

N-glycosylation site.

amino acids 130-134, 145-149, 217-221, 381-385

Casein kinase II phosphorylation site.

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,
384-388, 471-475, 481-485, 530-534

N-myristoylation site.

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

FIGURE 63

AGGCTCCGGCGGGCTGAGTGC GGACTGGAGTGGAAACCCGGTCCCCGGCTAGAGAACACGGC**A**TGACCA
CGTGGAGCCTCCGGCGAGGCCGGCCACGCTGGACTCCTGCTGGTCGTCTGGGCTCTGGTGCCTCC
GCAGGCTGGACTGGAGCACCCCTGGTCCCTCTGGGCTCCGCATCGACAGCTGGGCTGCAGGCCAAGGGCTGGA
ACTTCATGCTGGAGGATTCCACCTCTGGATCTTCGGGGCTCCATCAACTATTTCCGTGTGCCAGGGAGTACT
GGAGGGACCGCCTGCTGAAGATGAAGGCCTGTCGAACACCCCTACCACCTATGTTCCGTGGAACCTGCATG
AGCCAGAAAGAGCAAATTGACTTCTGGAACCTGGACTGGAGGCCTCGTCTGATGCCGCAGAGATCG
GGCTGTGGGTGATTCTGCGTCCAGGCCCTACATCTGCAGTGAGATGGACCTCGGGGCTTGCCAGCTGGCTAC
TCCAAGACCCCTGGCATGAGGCTGAGGACAACCTACAAGGGCTCACCGAAGCAGTGGACCTTATTTGACCACC
TGATGTCCAGGGTGGTGCACCTCCAGTACAAGCTGGGGACCTATCATTGCCGTGCAGGTGAGAATGAATATG
GTTCCATAATAAAGACCCGCATACATGCCCTACGTCAAGAAGGCACTGGAGGACCGTGGCATTGGAACACTGC
TCCTGACTTCAGACAACAAGGATGGGCTGAGCAAGGGATTGTCCAGGGAGTCTTGGCCACCATCAACTTGAGT
CAACACACGAGCTGCAGCTACTGACCACCTTCTTCAACGTCAGGGGACTCAGGCCAAGATGGTATGGAGT
ACTGGACGGGTGGTTGACTCGTGGGGAGGCCCTACAATATCTTGGATTCTCTGAGGTTTGAAAACCGTGT
CTGCCATTGTGGACGCCGGCTCCATCAACCTCTACATGTTCCACGGAGCACCAACTTGGCTTCATGAATG
GAGCCATGCACTTCCATGACTACAAGTCAGATGTCACCAGCTATGACTATGATGCTGTGCTGACAGAACCGGCG
ATTACACGCCAAGTACATGAAGCTCGAGACTTCTCGGCTCCATCTCAGGCATCCCTCCCTCCCCACCTG
ACCTTCTCCCAAGATGCCATGAGCCCTTAACGCCAGTCTGTACCTGTCTGTGGGACGCCCTCAAGTACC
TGGGGAGCCAATCAAGTCGAAAAGCCCACCAACATGGAGAACCTGCAGTCATGGGAAATGGACAGTCCT
TCGGGTACATTCTCATGAGACCAGCATCACCTCGTCTGGCATTCTCAGTGGCCACGTGCTGATCGGGGCG
TGTGGTGAACACAGTATCCATAGGATTCTGGACTACAAGACAACGAAGATTGCTGTGCTCCCTGATCCAGGGTT
ACACCGTGTGAGGATCTGGTGGAGAACATCGTGGCGAGTCAGTCAACTATGGGAGAATATTGATGACCAGGCCAAG
GCTTAATTGGAAATCTCATGTAATGATTCACTTCAACCTGAAAAAACTTCAGAATCTATAGCCTGGATATGAAGAAGA
GCTTCTTCAGAGGTTGGCCTGGACAAATGGNGTCCCTCCAGAAACACCCACATTACCTGTTCTTGG
GTAGCTTGTCCATCAGCTCACGCCCTGTGACACCTTCTGAGCTGGAGGGCTGGAGAAGGGGTTGATTCA
TCAATGGCCAGAACCTGGACGTTACTGGAACATTGGACCCAGAAGACGCTTACCTCCAGGTCCCTGGTGA
GCAGCGGAATCAACCAGGTATCGTTTGAGGAGACGATGGCGGCCCTGCATTACAGTTACGGAAACCCCC
ACCTGGCAGGAACAGTACATTAGT**G**AGCGTGGCACCCCTCTGCTGGTGCAGTGGAGACTGCCGCTC
CTCTTGACCTGAAGCCTGGCTGCTGCCACCCCTCACTGCAAAAGCATCTCTTAAGTAGCAACCTCAGGG
ACTGGGGCTACAGTCTGCCCTGTCTCAGCTAAAACCTAAGCCTGCAGGGAAAGGTGGGATGGCTCTGGGCC
TGGCTTGTGATGATGGCTTCTACAGCCCTGCTCTGTGCCAGGGCTGTCGGGCTGTCTAGGGTGGGAGC
AGCTAATCAGATGCCACGCCCTTGGCCCTCAGAAAAAGTGCCTGAAACGTGCCCTGCAACGGACGTACAGCCC
TGCAGCATCTGCTGGACTCAGCGTGTCTTGTGCTGGTCTGGGAGGCTTGGCACATCCCTCATGGCCCAT
TTTATCCCGAAATCTGGGTGTGTCACAGTGTAGAGGGTGGGAAGGGGTGTCTCACCTGAGCTGACTTTGTT
CTTCCTCACAAACCTCTGACGCCCTCTTGGGATTCTGAAGGAACCTGGCGTGAAGAACATGTGACTTCCCTT
TCCCTCCCACCGCTGCTTCCCACAGGGTGACAGGCTGGAGAACAGAAATCTCACCCCTGCGTCTTCC
CAAGTTAGCAGGTGTCTGGTGTTCAGTGAGGAGGACATGTGAGTCCCTGGCAGAACGCCATGCCCATGTCTGCA
CATCCAGGGAGGAGGACAGAACAGGCCAGCTCACATGTGAGTCCCTGGCAGAACGCCATGCCCATGTCTGCAACATCC
AGGGAGGAGGACAGAACAGGCCAGCTCACATGTGAGTCCCTGGCAGAACGCCATGCCCATGTCTGCAACATCCAGGG
GGAGGACAGAACAGGCCAGCTCACATGTGAGTCCCTGGCAGAACGCCATGCCCATGTCTGCAACATCCAGGGAGG
ACAGAACAGGCCAGCTCAGTGGCCCCGCTCCCAACCCCCCACGCCGAACAGCAGGGCAGAGCAGGCCCTCTC
GAAGTGTGTCAGTCCGCAAGTCCGCAATTGAGCCTGTTCTGGGGCCAGGCCAACACCTGGCTTGGGCTACTGTCTGA
GTTGCAGTAAAGCTATAACCTTGAATCACAA

FIGURE 64

MTTWSLRRR PART LGLLL VV LGFL VL RRL DWST LVPL RL RHRQL GLQAK GWN FM LED ST FW
IFGGSIHYFRVPREYWRDRLLKMKACGLNTLTTYVPWNLHEPERGKFDFSGNLDLEAFVLMA
AEIGLWVILRPGPYICSEMDLGGLPSWLLQDPGMRLRTTYKGFTEAVDLYFDHLMMSRVVPLQ
YKRGGPIIAVQVENEYGSYNKDPAYMPYVKKALEDRGIVELLTSNDKDGLSKGIVQGVLAT
INLQSTHELQLLTTFLNVQGTQPKMVMEYWTGFDSWGGPHNILDSSEVLKTVSAIVDAGS
SINLYMFHGGTNFGFMNGAMHFHDYKSDVTSYDYDAVLTEAGDYTAKYMKLRDFFGSISGIP
LPPPDLLPKMPYEPLTPVLYLSLWDALKYLGEPIKSEKPINMENLPVNGGNQSFYI LY
TSITSSGILSGHVHD RGQVFVN TVSIGFLDYKTTKIAVPLI QGYTVLRILVENRG RVNYGEN
IDDQRKGLIGNLYLNDSPLKNFRIYSLDM KKSFFQRFGLDKWXSLPETPTLPAFFLGSLSIS
STPCDTFLKLEGWEKGVVFINGQNLGRYWNIGPQKTL YLPGPW LSSGINQVIVFEETMAGPA
LQFTETPHLGRNQYIK

Signal sequence:

amino acids 1-27

Casein kinase II phosphorylation site.

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

N-myristoylation site.

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

FIGURE 65

GGGGACGCGGAGCTGAGAGGCTCCGGGCTAGCTAGGTGTAGGGGTGGACGGGTCCCAGGACC
CTGGTGAGGGTTCTACTTGGCCTTCGGTGGGGTCAAGACGCAGGCACCTACGCCAAAGG
GGAGCAAAGCCGGCTCGGCCGAGGCCCGAGGACCTCATCTCCAATGTTGGAGGAATC
CGACACGTGACGGTCTGTCCGCGTCTCAGACTAGAGGAGCGCTGTAAACGCC**ATGGCTCCC**
AAGAACGCTGTCCTGCCTCGTCCCTGCTGCGCTCAGCCTGACGCTACTGCTGCCCA
GGCAGACACTCGGTGCGTGTAGTGGATAGGGTCATGACCGGTTCTCCTAGACGGGGCCC
CGTTCGCTATGTGTGGCAGCCTGCACTACTTCGGGTACCGCGGGTGCTTGGGCCGAC
CGGCTTTGAAGATGCGATGGAGCGGCTCAACGCCATACAGTTATGTGCCCTGGAACTA
CCACCGAGCCACAGCCTGGGTCTATAACTTAATGGCAGCCGGACCTCATTGCCTTCTGA
ATGAGGCAGCTCTAGCGAACCTGTTGGTCATACTGAGACCAGGACCTTACATCTGTGCAGAG
TGGGAGATGGGGGTCTCCATCCTGGTTGCTCGAAAACCTGAAATTCTAAGAACCTC
AGATCCAGACTTCCCGCAGTGGACTCCTGGTTCAAGGTCTGCTGCCAAGATATATC
CATGGCTTATCACAATGGGGCAACATCATTAGCATTAGCTAGGAGAATGAATATGGTAGC
TACAGAGCCTGTGACTTCAGCTACATGAGGCACTTGGCTGGCTTCCGTGCACTGCTAGG
AGAAAAGATCTTGCTCTCACACAGATGGGCTGAAGGACTCAAGTGTGGCTCCCTCCGGG
GAECTATACCACTGTAGATTTGGCCAGCTGACAACATGACCAAAATCTTACCTGCTT
CGGAAGTATGAACCCCATTGGCATTGGTAAACTCTGAGTACTACACAGGCTGGCTGGATT
CTGGGGCCAGAATCACTCCACACGGTCTGTGTCAGCTGTAACCAAAGGACTAGAGAACATGC
TCAAGTTGGAGGCCAGTGTGAACATGTACATGTTCCATGGAGGTACCAACTTGGATATTGG
AATGGTGCCGATAAGAACGGGACGCTTCCCTCGATTACTACCAGCTATGACTATGATGCACC
TATATCTGAAGCAGGGGACCCACACCTAACGTTAGCTTGTGAGATGTCATCAGCAAGT
TCCAGGAAGTCCCTGGACCTTACCTCCCCGAGCCCCAAGATGATGCTTGGACCTGTG
ACTCTGCACCTGGTGGCATTACTGGCTTCTAGACTTGCTTGCCTGGCTGGACCTGT
TCATTCAATCTGCCAATGACCTTGAGGCTGTCAAGCAGGACCATGGCTCATGTTGACC
GAACCTATATGACCCATACCATTGGAGCCAACACCATTCTGGTGCCAAATAATGGAGTC
CATGACCGTGCCTATGTGATGGTGGATGGGTGTTCCAGGGTGTGGAGCGAAATATGAG
AGACAAACTATTTTGACGGGAAACTGGGTCAAACACTGGATATCTGGTGGAGAACATGG
GGAGGCTCAGCTTGGGTCTAACAGCAGTGACTTCAAGGGCCTGTTGAAGCCACCAATTCTG
GGGCAAACAATCCTTACCCAGTGGATGATGTTCCCTCTGAAAATTGATAACCTTGTGAAGTG
GTGGTTCCCTCCAGTTGCCAAATGCCATATCCTCAAGCTCCTCTGGCCCCACATTCT
ACTCCAAAACATTCCAATTAGGCTCAGTGGGGACACATTCTATATCTACCTGGATGG
ACCAAGGGCCAAGTCTGGATCAATGGTTAACATTGGGCCGGTACTGGACAAAGCAGGGCC
ACAACAGACCTCTACGTGCCAAGATTCCCTGCTGTTCCATGGGAGCCCTAACAAAATTA
CATTGCTGGAACTAGAACATGTACCTCTCCAGCCCCAAGTCCAATTGGATAAGCTATC
CTCAATAGCACTAGTACTTGCACAGGACACATATCAATTCCCTTCAGCTGATACACTGAG
TGCCTCTGAACCAATGGAGTTAAGTGGGACT**GAAAGGTAGGCCGGCATGGCTCATGC**
CTGTAATCCCAGCACTTGGGAGGCTGAGACGGGTGGATTACCTGAGGTCAAGGACTTCAAGA
CCAGCCTGGCCAACATGGTAAACCCGTCTCCACTAAAAATACAAAATTAGCCGGCGTG
ATGGTGGGCACCTCTAACATCCCAGCTACTTGGGAGGCTGAGGGCAGGAGAATTGCTGAATCC
AGGAGGCAGAGGTTGCAGTGAGTGGAGGTTGTACCACTGCACTCCAGCCTGGCTGACAGTGA
GACACTCCATCTCAAAAAAAAAAA

FIGURE 66

MAPKKLSCLRSLLLPLSLTLLLPQADTRSFVVDRGHDRFLLDGAPFRYVSGSLHYFRVPRVL
WADRLLKMRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYI
CAEWEMGGGLPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNIISIQVENE
YGSYRACDFSYMRHLAGLFRAALLGEKILLFTTDGPEGLKCGSLRGLYTTVDFGPADNMTKIF
TLLRKYEPHGPLVNSEYYTGWLWQNHSRSVSAVTKGLENMLKLGA
SVNMYMFHGGTNF
GYWNGADKKGRFLPITTSDYDAPISEAGDPTPKLFALRDVISKFQEVP
LGPLPPSPKMML
GPVTLHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMTH
TIFEPTPFWVPN
NGVHDRAYVMVDGVFQGVVERNMRDKLFLTGKLGSKLDILVENMGR
LSFGSNSSDFKGLLKP
PILGQTILTQWMMFPLKIDNLVKWWFPLQLPKWPYPQAPSGPTFYSKTF
PILGSVGDTFLYL
PGWTKGQVWINGFNLGRYWTQGPQQTLYVPRFLLFPRGALNKITLLE
LEDVPLQPQVQFLD
KPILNSTSTLHRTHINSLSADTLSASEPMELSGH

Signal sequence:

amino acids 1-27

N-glycosylation site.

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 4-8

Casein kinase II phosphorylation site.

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,
603-607, 644-648

Tyrosine kinase phosphorylation site.

amino acids 191-198

N-myristoylation site.

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

FIGURE 67

GCTTGAACACGTCTGCAAGCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTCAGTGC
ACCCACAATATGGCTTACATGTTAAAAAGCTTCTCATCAGTTACATATCCATTATTTGTGT
TTATGGCTTATCTGCCTCTACACTCTCTGGTTATTCAAGGATACCTTGAAAGGAATATT
CTTCGAAAAGTCAGAGAAGAGAGCAGTTAGTGACATTCCAGATGTCAAAACGATTT
GCGTTCTTCTCACATGGTAGACCAGTATGACCAGCTATATTCCAAGCGTTGGTGTGTT
CTTGTCAAGAGTTAGTGAAAATAACTTAGGAAATTAGTTGAACCATGAGTGGACATTG
AAAAACTCAGGCAGCACATTCAACGCCAGGACAAGCAGGAGTTGCATCTGTTCATG
CTGTCGGGGGTGCCGATGCTGTCTTGACCTCACAGACCTGGATGTGCTAAAGCTTGAACT
AATTCCAGAAGCTAAAATTCTGCTAACAGATTCTCAAATGACTAACCTCCAAGAGCTCCACC
TCTGCCACTGCCCTGCAAAAGTTGAACAGACTGCTTTAGCTTCTCGCGATCACTTGAGA
TGCCTTCACGTGAAGTTCACTGATGTGGCTGAAATTCTGCCTGGGTGTATTGCTAAAAAA
CCTTCGAGAGTTGTACTTAATAGGCAATTGAACACTGAAAACAATAAGATGATAGGACTTG
AATCTCTCCGAGAGTTGCGGCACCTTAAGATTCTCACGTGAAGAGCAATTGACCAAAGTT
CCCTCCAACATTACAGATGTGGCTCCACATCTAACAAAGTTAGTCATTCTAACATGACGGCAC
TAAACTCTGGTACTGAACAGCCTTAAGAAAATGATGAATGTCGCTGAGCTGGAACTCCAGA
ACTGTGAGCTAGAGAGAATCCCACATGCTATTTCAGCCTCTAACAGGAACGGAT
TTAAAGTCCAATAACATTGCAACAATTGAGGAAATCATCAGTTCCAGCATTAAAACGACT
GACTTGTAAATTATGGCATAACAAAATTGTTACTATTCCCTCCCTATTACCCATGTCA
AAAACTTGGAGTCACTTATTCTAACACAAGCTCGAACCTTACAGTGGCAGTATT
AGTTACAGAAAACTCAGATGCTTAGATGTGAGCTACAACAAACATTCAATGATTCAATAGA
AATAGGATTGCTTCAGAACCTGCAGCATTGCATATCACTGGAAACAAAGTGGACATTCTGC
CAAAACAATTGTTAAATGCATAAAGTTGAGGACTTGAATCTGGACAGAACTGCATCACC
TCACTCCCAGAGAAAGTTGGTCAGCTCTCCAGCTCACTCAGCTGGAGCTGAAGGGAACTG
CTTGGACCGCCTGCCAGCCCAGCTGGGCCAGTGTGGATGCTCAAGAAAAGCGGGCTTGTG
TGGAAGATCACCTTTGATAACCTGCCACTCGAACAGTCAAAGAGGCATTGAATCAAGACATA
AATATTCCCTTGCAAATGGATTTAAACTAAGATAATATGCACAGTGATGTGCAGGAAC
AACTCCTAGATTGCAAGTGCTCACGTACAAGTTATTACAAGATAATGCATTAGGAGTAG
ATACATCTTTAAAATAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT
GTTCAATGTTGAGGGTTAAAGTCATTCAATCATAATCATTGTTCTTTAAATTGTTGTAACGGAT
GCTGCCGCTACTGAATGTTACAAATTGCTTGCTGCTAAAGTAAATGATTAATTGACATT
TTCTTACTAAAAAAAAAAAAAA

FIGURE 68

MAYMLKKLLISYISIICVYGFICLYTLFWLFRIPLKEYSFEKVREESSFSDIPDVKNDFAFL
LHMVDQYDQLYSKRGVFLSEVSENKLREISLNHEWTFEKLQRQHISRNAQDKQELHLFMLSG
VPDAVFDLTDLDVLKLELIPEAKIPAKISQMNTNLQELHLCHCPAKVEQTAFSFLRDHLRCLH
VKFTDVAEI PAWVYLLKNLRELYLIGNLNSENNKMIGLESLRELRLKILHVKSNLTKVPSN
ITDVAPHLTKLVIHNDGTKLLVLNSLKKMMNVAELELQNCELERIPHAI FSLSNLQELDLKS
NNIRTIEEIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESLYFSNNKLESLPVAVFSLQ
KLRCLDVSYNNISMPIEIGLLQNLQHLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLP
EKVGQLSQLTQLELKGNCLDRPAQLGQCRMLKKSGLVVEDHLFDTLPLEVKEALNQDINIP
FANGI

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 241-245, 248-252, 383-387

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 326-330

Casein kinase II phosphorylation site.

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

Tyrosine kinase phosphorylation site.

amino acids 349-355, 375-381

N-myristoylation site.

amino acids 78-84, 124-130, 212-218, 392-398

FIGURE 69

CCACCGCGTCCGGCCTCTCTGGACTTTGCATTCCATTCTTCATTGACAAACTGACTTTTTATTTCT
TTTTTCCATCTCTGGGCAGCTTGGGATCCTAGGCCCTGGGAAGACATTGTGTTTACACACATAAGGAT
CTGTGTTGGGTTCTTCTCCTCCCTGACATTGGCATTGCTTAGTGGTGTGGGGAGGGAGACCGACGTGG
GCTCAGTGCTTGCTGCACTTATCTGCTTAGGTACATCGAAGTCTTGACCTCCATACAGTGATTATGCCTGTC
ATCGCTGGTGGTATCCTGGCGCTTGCTCCTGCTGATAGTGTGCTCTGTCTTACTTCAAATACACAAC
GCGCTAAAAGCTGCAAAGAACCTGAAGCTGTGGCTGAAAAAATACAACCCAGACAAGGTGTGGTGGGCCAAG
AACAGCCAGGCCAAACCATGCCACGGAGTCTGTGCTGCCCTGAGTGTGAAGGATATAGAATGTGTGCC
AGTTTGATTCCCTGCCACCTTGCTGTCGACATAAATGAGGGCCTTGAGTTAGGAAAGGCTCCCTCTCAA
GCAGAGCCCTGAAGACTCAATGATGTCATGAGGCCACCTGTTGTGATGTGCAGGCACAGAAGAAAGGCACAG
CTCCCCATCAGTTCATGAAAATAACTCAGTGCTGTGGACCAGCTGCTGGAGATCCCTACAGAGAGCTTC
CACTGGGGCAACCCCTCAGGAAGGAGTTGGGAGAGAGAACCCACTGTGGGAATGCTGATAAACCCAGTC
CACAGCTGCTCTATTCTCACACAAATCTACCCCTGCGTGGCTGAACTGACGTTCCCTGGAGGTGTCAGAAA
GCTGATGTAACACAGAGCTATAAAAGCTGTGGCTCTAAGGCTGCCAGGCCCTGCAAATGGAGCTTGTA
AGAAGGCTCATGCCATTGACCCCTCTAATTCTCTGTGTTGGGGAGCTGACATGGCGAGGCTGAAGGCAAT
GCAAGCTGCACAGTCAGTCTAGGGGGTGCCTAATGGCAGAGACCCACAAAGCCATGATCTGCAACTCAATCCC
AGTGAGAACTGCACCTGGACAATAGAAAAGACAGAAAACAAAGCATCAGAATTATCTTCTATGTCAGCTT
GATCCAGATGGAAGCTGTGAAAAGTGAAAACATTAAAGTCTTGACGGAACCTCCAGCAATGGGCTCTGCTAGGG
CAAGTCTGAGTAAAACAGACTATGTCCTGTATTGAAATCATCATCCAGTACATTGACGTTCAAATAGTTACT
GACTCAGCAAGAATTCAAAGAACTGTCTTGTCTACTACTCTCTCTCCTAAACATCTCTATTCCAAACTGT
GGCGTTACCTGGATACCTTGGAGGATCCTTCACCAGCCCAATTACCCAAGCCGATCTGAGCTGGCTTAT
TGTGTGGCACATACAAGTGGAGAAAGATTACAAGATAAAACTAAACCTCAAAGAGATTTCCTAGAAATAGAC
AAACAGTGCACAAATTGATTTCCTGCCATCTATGATGGCCCCTCCACCAACTCTGGCTGATTGGACAAGTCTGT
GGCGTGTGACTCCCACCTCGAATCGTCATCAAACCTCTGACTGTGTTGCTACAGATTATGCCAATTCT
TACCGGGGATTTCCTGCTCTCACACCTCAATTATGAGAAAACATCAACACTACATCTTAACCTGCTCT
GACAGGATGAGAGTTATTATAAGCAAATCCTACCTAGAGGCTTTAACTCTAATGGGATAACTTGCAACTAAA
GACCCAACCTGAGACCAAAATTATCAAATGTTGGAATTTCCTGCCCTCTTAATGGATGTGGTACAATCAGA
AAGGTAGAAGATCAGTCACCAATTACACCAATAATCACCTTCTGCATCTCAACTCTGAAGTGTACCC
CGTCAGAAACAACCTCCAGATTATGTGAAGTGTGAAATGGGACATAATTCTACAGTGGAGATAATATACATAACA
GAAGATGATGTAATACAAAGTCAAATGCACCTGGCAAATATAACACCCAGCATGGCTTTGAATCCAATTCA
TTTGAAGACTATACTGAATCACCATTATGTTGAAACCAACTCTTTGTTCAAGTTAGTCTGCAC
ACCTCAGATCCAAATTGGTGGTCTTGATACCTGTAGAGCCTCTCCACCTGACTTTGCATCTCCAACC
TACGACCTAATCAAGAGTGGATGTAGTCGAGATGAAACTGTGAGGTGATCCCTTATTGACACTATGGGAGA
TTCCAGTTAACGCTTTAAATTCTTGAGAAGTATGAGCTCTGTGATCTGCAGTGTAAAGTTTGATATGTGAT
AGCAGTGACCACCGACTCGCTGCAATCAAGGTTGTGCTCCAGAAGCAGAGACATTCTTCATATAATGG
AAAACAGATTCCATCATAGGACCCATTGCTGAAAGGAGTCGAAGTGCAGTGGCAATTCAAGGATTTCAGCAT
GAAACACATGGGAAGAAACTCCAAACCCAGCCTTCAACAGTGTGACATTGTTCTCATGGTTCTAGCTCTG
AATGTGGTGAATGTCAGCGACAATCACAGTGGCATTGAAATCAACGGGAGACTACAAATACCAAGAAGCTG
CAGAACTATTAACTAACAGGTCCAACCCCTAAGTGAGACATGTTCTCAGGATGCCAAAGGAAATGCTACCTCGT
GGCTACACATATTATGAAATAATGAGGAAGGGCTGAAAGTGACACACAGGCCTGATGTA

FIGURE 70

MELVRRLMPLTLLIISCLAE LTMAEAEGNASCTVSLGGANMAETHKAMILQLN PSENCTWTI
ER PENKSIRIIFSYVQLDPDGSESENIVFDGTSSNGP LQVCSKNDYVPFESSSTLT
FQIVTDSARIQRTVFVFFSPNISIPNCGGYLDTLEGSFTSPNPKPHPELAYCVWHIQV
EKDYKIKLNFKEIFLEIDKQCKFDLAIYDGPSTNSGLIGQVCGRVTPTFESSSNSLTVVLS
TDYANSYRGFSAS YTSIYAENINTTSLTCSSDRMRVIISKSYLEAFNSNGNNLQLKDPTCRP
KLSNVVEFSVPLNGCGTIRKVEDQSIYTNIITFSASSTSEVITRQKQLQIIVKCEMGHNST
VEIIYITEDDV IQSQNALGKYNTSMALFESNSFEKTI LESPYV DLNQTLFVQVSLHTSDPN
LVVFLDTCRASPTSDFASPTYDLIKSGCSRDETCKVYPLFGHYGRFQFN AFKFLRSMSSVYL
QCKVLICDSSDHQSRCNQGC VSR SKRD ISSYKW KTD SII GPIRLKRDRSASGN SGFQHETHA
EETPNQPFNSVHLFSFMVLALNVVT VATITVRHFVNQRADYKYQKLQNY

Signal sequence:

amino acids 1-24

Transmembrane domain:

amino acids 571-586

N-glycosylation site.

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,
394-398, 419-423

Casein kinase II phosphorylation site.

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,
408-412, 463-467, 520-524, 556-560

Tyrosine kinase phosphorylation site.

amino acids 172-180, 407-415, 407-416, 519-528

N-myristoylation site.

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 71

GACGGAAGAACAGCGCTCCCGAGGCCGCCGGAGCTGCAGAGAGGACAGCCGGCCTGCAGCG
GGACATGCAGGCCAGGAGCTCCCCAGGCTCGCGTCTCCGTTGCTGTTGCTGTTGCTGC
TGCTGCCGCCGCCGTGCCCTGCCACAGCGCACGCCAGCTGTTGACCAGGCAAGTCGGCATCTTCATCCACTG
CTGGACGCCGCCAGCTGCCCGCTGGTTGAGCTGGTAGCGAGTGGTCTGGTGGATTGGCAAAAGGAAA
AGATAACCGAAGTATGTGAAATTATGAAAGATAATTACCCCTCTAGTTCAAAATATGAAGAT
TTTGGACCACTATTACAGCAAAATTGTTAATGCCAACAGTGGGCAGATATTTCAGGC
CTCTGGTGCCAAATACATTGTCTTAACCTCAAACATCATGAAGGCTTACCTTGTTGGGGGT
CAGAATATTGGAACGGATGCCATAGATGAGGGGCCAAGAGGGACATTGTCAGGAA
CTTGAGGTAGCCATTAGGAACAGAACTGACCTGCGTTGGACTGTACTATTCCCTTTGA
ATGGTTCATCGCTCTCCTGAGGATGAATCCAGTTCCATAAGCGGAATTCCAG
TTTCTAAGACATTGCCAGAGCTCTATGAGTTAGTGAACAACATATCAGCCTGAGGTTCTGTGG
TCGGATGGTGACGGAGGAGCACCGGATCAAACTCGAACAGCACAGGCTCTGGCTGGTT
ATATAATGAAAGCCCAGTCGGGCACAGTAGTCACCAATGATCGTTGGGAGCTGGTAGCA
TCTGTAAGCATGGTGGCTCTATACCTGAGTGTATAACCCAGGACATCTTGCCA
CATAAATGGAAAAGTGCATGACAATAGACAAACTGTCCTGGGCTATAGGAGGGAAGCTGG
AATCTCTGACTATCTACAATTGAAGAATTGGTGAAGCAACTGTAGAGACAGTTCATGTG
GAGGAAATCTTGATGAATATTGGGCCACACTAGATGGCACCATTCGTAGTTTGAG
GAGCGACTGAGGAAGTGGGCTCTGGCTAAAGTCAATGGAGAAGCTATTATGAAACCTA
TACCTGGCGATCCCAGAATGACACTGTCACCCAGATGTGTGGTACACATCCAAGCCTAAAG
AAAAATTAGTCATGCCATTCTAAATGGCCACATCAGGACAGCTGTTCTGGCAT
CCCAAAGCTATTCTGGGGCAACAGAGGTGAAACTACTGGCCATGGACAGCCACTTAACG
GATTCTTGAGCAAATGGCATTATGGTAGAACTGCCACAGCTAACCATTCAGATGC
CGTGTAAATGGGCTGGCTAGCCCTAACTAATGTGATCTAAAGTGCAGCAGAGTGGCTG
ATGCTGCAAGTTATGTCTAAGGCTAGGAACATCAGGTGTCATAATTGTTAGCACATGGAGA
AAGCAATGTAACCTGGATAAGAAAATTATTGGCAGTTCCAGGCCCTTCCCTTCCACTA
AATTCTTCTAAATTACCCATGTAACCATTAACTCTCCAGTGCACCTGGCATTAAAGTC
TCTTCACATTGATTGTTCCATGTGACTCAGAGGTGAGAATTTCACATTATAAGTAG
CAAGGAATTGGGGTATTATGGACCGAAGTGAACATTGTTGAAGCCATATCCCCCATG
ATTATATAGTTATGCATCACTTAATATGGGGATATTCTGGGAAATGCATTGCTAGTCAT
TTTTTTGTGCCAACATCATAGAGTGTATTACAAACCTAGATGGCATAGCCTACTACA
CACCTAATGTGATGGTATAGACTGTTGCTCTAGGCTACAGACATATACAGCATGTTACTG
AATACTGTAGGCAATAGTAACAGTGGTATTGTATATGAAACATATGGAAACATAGAGAAG
GTACAGTAAAATACTGTAATGGTGCACCTGTATAGGGCACTTACCGAATGGAG
CTTACAGGACTGGAAGTGTCTGGTGAGTCAGTGAATGTGAAGGCCAGGACATTA
TTGAACACTGCCAGACGTTATAAAACTGTATGCTTAGGCTACACTACATTATAAAAAAAA
GTTTTCTTCTCAATTATAAACTAACATAAGTGTACTGTAACATTACAAACGTTTAATT
TTTAAACCTTTGGCTTTGTAAACACTTAGCTAAACATAAAACTCATTGTGCAA
ATGTAA

FIGURE 72

MRPQELPRLAFPLLLLLLPPPPCPAHSATRFDPTWESLDARQLPAWFDQAKFGIFIFHWG
VFSVPSFGSEWFWWYQKEKIPKYVEFMKDNYPPSFKYEDFGPLFTAKFFNANQWADIFQAS
GAKYIVLTSKHHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAIRNRTDLRGFLYYSLFEW
FHPLFLEDESSSFHKRQFPVSKTLPELYELVNYYQPEVLWSDGDGGAPDQYWNSTGFLAWLY
NESPVRGTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYRREAGI
SDYLTTIEELVKQLVETVSCGGNLLMNIGPTLDGTISVVFEERLRQVGSLKVNGEAIYETYT
WRSQNDTVTPDVWYTSPKPEKLVYAIFLKWPTSGQLFLGHPKAILGATEVKLLGHGQPLNWI
SLEQNGIMVELPQLTIHQMPCKWGWALALTNVI

Signal sequence:

amino acids 1-28

N-glycosylation site.

amino acids 171-175, 239-243, 377-381

Casein kinase II phosphorylation site.

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,
375-375

Tyrosine kinase phosphorylation site.

amino acids 361-369, 389-397

N-myristoylation site.

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

Leucine zipper pattern.

amino acids 410-432

Alpha-L-fucosidase putative active site.

amino acids 283-295

FIGURE 73

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTAACATAGT
TCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAAGTGGCCATC
TGAGGTGTTCCCTGGCTCTGAAGGGTAGGCACGATGCCAGGTGCTTCAGCCTGGTGTG
CTTCTCACTCCATCTGGACCACGAGGCTCTGGCCAAGGCTTTGCGTGCAGAAGAGCT
TTCCATCCAGGTGTCATGCAGAATTATGGGATCACCTGTGAGCAAAAGGCGAACCGAC
AGCTGAATTTCACAGAAGCTAAGGAGGCTGTAGGCTGCTGGACTAAGTTGGCCGGCAAG
GACCAAGTTGAAAACAGCCTGAAAGCTAGCTTGAAACTTGCAGCTATGGCTGGGTGGAGA
TGGATTCGTGGTCATCTCTAGGATTAGCCAAACCCCAAGTGTGGGAAAATGGGTGGGTG
TCCTGATTGGAAGGTTCCAGTGAGCCGACAGTTGCAGCCTATTGTTACAACACTCATCTGAT
ACTTGGACTAACCTGTCATCCAGAAATTATCACCACCAAAGATCCCATTCAACACTCA
AACTGCAACACAAACACAAGAATTATTGTCACTGACAGTACCTACTCGGTGGCATCCCCTT
ACTCTACAATACCTGCCCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGG
AGAAAAAAATTGATTGTGTACAGAAGTTTATGAAACTAGCACCAGTCTACAGAAC
TGAACCATTGTTGAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTGGAGGTGTCC
CCACGGCTCTGCTAGTGCTCTCCCTTTACAAACAAGAATCAGCAGAAGGAAATGAT
TATGTCAAAAGGTATGTGAAGGCCTTCCCTTTACAAACAAGAATCAGCAGAAGGAAATGAT
CGAAACCAAAGTAGTAAAGGAGGAGAAGGCCATGATAGCAACCTAATGAGGAATCAAAGA
AAACTGATAAAACCCAGAACAGAGTCCAAGAGTCCAAGAAAATACCGTGCATGCTGGAA
GCTGAAGTTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTCTTCATGCTCC
TTACCCCTGCCAGCTGGGAAATCAAAGGCCAAAGAACCAAAGAACGAAAGTCCACCCCTT
GGTTCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAAGAAC
CCTTCTCCTATTGTAACCCCTGCTGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGGCC
TTCTAGCCTGGCTATGTCCTAATAATATCCCACGGAGAAAGGAGTTTGCAAAAGTCAA
GGACCTAAACATCTCATCAGTATCCAGTGGTAAAAGGCCCTGGCTGTGAGGCTAGG
TGGGTGAAAGCCAAGGAGTCAGTGGACAGAACGGCTTCTACTGATTCCGAGCTCAGAC
CCTTCTCAGCTCTGAAAGAGAACACGTATCCCACCTGACATGCTCTGAGCCCGGTA
AGAGCAAAGAACGGAGAAAAGTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAG
ACCTAATCTCTGTAAGCTAAAATAAAGAAATAGAACAAAGCTGAGGATACGACAGTACACT
GTCAGCAGGACTGTAAACACAGACAGGGTCAAAGTGTGTTCTGAAACACATTGAGTTGGA
ATCACTGTTAGAACACACACACTTACTTTCTGGTCTCTACCACTGCTGATATTCTCT
AGGAAATATACTTTACAAGTAACAAAATAAAGACTCTTATAAAATTCTATTCTATCTGA
GTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTGTTAAAAGTAATAAAATTCA
ACAAACATTGCTGAATAGCTACTATATGTCAGTGCTGCAAGGTATTACACTCTGTAAT
TGAATATTATTCTCAAAAATTGCACATAGTAGAACGCTATCTGGGAAGCTATTTCT
GTTTGATATTCTAGCTTACTCTCCAAACTAATTGTTATTGCTGAGACTAATCT
ATTCAATTCTCTAATATGCCAACATTATAACCTTAATTATTATTAAACATACTAAGAAC
TACATTGTTACCTCTATACCAAGCACATTAAAAGTGCCATTAACAAATGTACTCA
GCCCTCTTTCCAACAAGAAGGGACTGAGAGATGCAGAAATATTGTCAGAAATTAA
AGCATTAGAAAATT

0 9 9 9 0 0 2 4 2 0 2 4 0 0

FIGURE 74

MARCFSLVLLTSIWTTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACR
LLGLSLAGKDQVETALKASFETCSYGVGDGFVVISRISPNNPKCGKNGVGVLIWKVPVRQF
AAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPP
APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAASKNEAAGFGGVPTALLVLALLFF
GAAAGLGFCYVKRYVKAFTPNTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSP
SKTTVRCLEAEV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 53-57, 130-134, 289-293

Casein kinase II phosphorylation site.

amino acids 145-149, 214-218

Tyrosine kinase phosphorylation site.

amino acids 79-88

N-myristoylation site.

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

FIGURE 75

AGATGGCGGTCTTGGCACCTCTAATTGCTCTCGTATTGGTGCCTCGACTTCACGATGG
CTGCCAACCTTAACCTCTGCTCGGCCCTGCTCTGCTGCCTCCTACTCGTGAGGAA
ACTGCCGCCCTGCCACGGCTGCCACCCAACGCGAAGACGGTAACCGTGTGACTTTG
ACTGGAGAGAAGTGGAGATCCTGATGTTCTCAGTGCATTGTGATGATGAAGAACCGCAGA
TCCATCACTGTGGAGCAACATATAAGGCAACATTTCATGTTAGTAAAGTGGCCAACACAAT
TCTTTCTTCCGCTTGGATATTGCATGGCCTACTTACATCACACTCTGCATAGTGTCC
TGATGACGTGCAAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAA
ACCATTGATGAGGAACTAGAACGGACAAGAGGGTCACTTGGATTGGAGTTCTTGCCAA
TTGGTCTAATGACTGCCAACATCATTGCCCTATCTATGCTGACCTCCCTAAATACAAC
GTACAGGGCTAAATTTGGAGGTGGATGTTGGACGCTATACTGATGTTAGTACGCCGTAC
AAAGTGAGCACATCACCCCTCACCAAGCAACTCCCTACCCCTGATCCTGTTCCAAGGGCAA
GGAGGCAATGCCGGGCCACAGATTGACAAGAAAGGACGGCTGTCATGGACCTCTCTG
AGGAGAATGTGATCCGAGAATTAACTTAAATGAGCTATAACCAGCGGGCCAAGAAACTATCA
AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTTCAACCCCCACCAAGTGTCA
TGGGAAAACAAGAAGGATAAATAAGATCCTCACTTGGCAGTGCTCCTCCTGTCAATT
CCAGGCTTTCCATAACCACACAAGCCTGAGGCTGCAGCCTTNATTNATGTTTCCCTTGG
CTGNGACTGGNTGGGGCAGCATGCAGCTCTGATTAAAGAGGCATCTAGGAAATTGTCAG
GCACCCCTACAGGAAGGCCTGCCATGCTGGCCAAGTTCACTGGAGCAAGAAAGAGATC
TCATAGGACGGAGGGGAAATGGTTCCCTCAAGCTTGGTCAGTGTGTTAACTGCTTATC
AGCTATTCAAGACATCTCCATGGTTCTCCATGAAACTCTGTTGTTCATCATTCTCTTAG
TTGACCTGCACAGCTTGGTTAGACCTAGATTAAACCTAAGGTAAGATGCTGGGTATAGAA
CGCTAAGAATTTCACCCCAAGGACTCTGCTTCAAGCCCTCTGGCTTCGTTATGGTC
TTCATTAAAAGTATAAGCCTAACCTTGTGCTAGTCCTAAGGAGAAACCTTAACCACAAAG
TTTTTATCATTGAAGACAATATTGAACAAACCCCTATTGTGGGATTGAGAAGGGGTGAA
TAGAGGCTTGAGACTTTCTTGTGTGGTAGGACTGGAGGAGAAACCTGGACTTCA
TAACCCCTCTGACATACTCCCCACACCCAGTTGATGGCTTCCGTAATAAAAGATTGGGATT
TCCTTTTG

FIGURE 76

MAVLAPLIALVYSVPRLSRWLAQPYYLLSALLSAAFLLVRKLPPCHGLPTQREDGNPCDFD
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMF SKVANTILFFRLDIRMGLLYITLCIVFL
MTCKPPLYMGPEYIKYFNDKTIDEELERDKRTWIVEFFANWSNDCQSFAPIYADLSLKYNC
TGLNFGKVDVGRYTDVSTRYKVSTSPLTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE
ENVIREFNLNELYQRACKLSKAGDNIPPEEQPVASTPTVSDGENKKDK

Signal sequence:

amino acids 1-48

Transmembrane domain:

amino acids 111-125

N-glycosylation site.

amino acids 165-169, 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 154-158, 265-269

Casein kinase II phosphorylation site.

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

N-myristoylation site.

amino acids 188-194, 225-231

Myb DNA-binding domain repeat signature 1.

amino acids 244-253

FIGURE 77

GGACAGCTCGCGCCCCCGAGAGCTTAGCCGTGAGGAGCTGCCTGGGACGTTGCCCTG
GGGCCAGCCTGGCCGGTCACCCTGGCATGAGGAGATGGCCTGTTGCTCCTGGTCCA
TTGCTCCTGCTGCCGGCTCCTACGGACTGCCCTCTACAACGGCTCTACTACTCCAACAG
CGCCAACGACCAGAACCTAGGCAACGGTCATGGCAAAGACCTCCTTAATGGAGTGAAGCTGG
TGGTGGAGACACCCGAGGGAGACCTGTTCACCTACCAAGGGGCCAGTGTGATCCTGCCCTGC
CGCTACCGCTACGAGCCGGCCCTGGTCTCCCGCGCGTGTGCGTGTCAAATGGTGAAGCT
GTCGGAGAACGGGGCCCCAGAGAAGGACGTGCTGGCATCGGCTGAGGCACCGCTCCT
TTGGGACTACCAAGGCCGCGTGCACCTGCGCAGGACAAAGAGCATGACGTCTCGCTGGAG
ATCCAGGATCTGCGCTGGAGGACTATGGCGTTACCGCTGTGAGGTCAATTGACGGCTGGA
GGATGAAAGCGGTCTGGTGGAGGCTGGAGCTGCGGGGTGTGGCTTTCCCTACCAGTCCCCCA
ACGGCGCTACCAGTTCAACTTCCACGAGGGCCAGCAGGTCTGTGCAAGAGCAGGCTGCCGTG
GTGGCCTCCTTGAGCAGCTTCCGGCCTGGAGGAGGGCCTGGACTGGTGCAACGCCGG
CTGGCTGCAGGATGCTACGGTGCAGTACCCCCTCATGTTGCCCGGCAGCCCTGCCGTGGCC
CAGGCCTGGCACCTGGCGTGCAGCTACGGCCCCGCCACCGCCGCTGCACCGCTATGAT
GTATTCTGCTCGCTACTGCCCTCAAGGGCGGGTGTACTACCTGGAGCACCTGAGAAGCT
GACGCTGACAGAGGCAAGGGAGGCCTGCCAGGAAGATGATGCCACGATGCCAAGGTGGAC
AGCTTTGCCGCTGGAAGTTCCATGGCCTGGACCGCTGCCACGCTGGCTGGCTGGCAGAT
GGCAGCGTCCGCTACCCCTGTGGTTACCCGCATCTAACTGTGGCCCCCAGAGCCTGGGT
CCGAAGCTTGGCTTCCCCGACCCGCAGAGCCGCTTGTACGGTGTACTGCTACCGCCAGC
ACTAGGACCTGGGCCCTCCCGCCATTCCCTACTGGCTGTGATTGAGTGGTT
CGTTTCCCTGTGGGTTGGAGCCATTTAACTGTTTATACTTCTCAATTAAATTCT
TTAAACATTTTTACTATTTTGAAAGCAAACAGAACCCATGCCCTCCCTTGCTCCTG
GATGCCCACTCCAGGAATCATGCTGCTCCCTGGCCATTGCGGTTTGAGGCTCTG
GAGGGTTCCCGCCATCCAGGCTGGCTCCCTCCCTTAAGGAGGTTGGTGCAGAGTGGC
GGTGGCCTGTCTAGAATGCCGCCGGAGTCCGGCATGGGGCACAGTTCTCCCTGCCCT
CAGCCTGGGGAAAGAAGAGGGCCTGGGGCTCCGGAGCTGGCTTGGCCTCTCCTGCC
CACCTCTACTCTGTGAAGCCGCTGACCCCAGTCTGCCACTGAGGGCTAGGGCTGGAA
GCCAGTTCTAGGCTTCCAGGCAGAATCTGAGGGAAAGGAAGAAACTCCCTCCCCGTTCCCT
TCCCTCTCGGTTCAAAGAAATCTGTTGTCATTGTTCTCTGTTCCCTGTGTGG
GGAGGGGCCCTCAGGTGTGTACTTGGACAATAATGGTGTATGACTGCCTCCGCCAA
AAA
AAA

FIGURE 78

MGLLLLVPLLLLPGSYGLPFYNGFYYNSNSANDQNLGNHGKDLLNGVKLVVETPEETLFTYQ
GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLVAIGLRHRSFGDYQGRVHLRQD
KEHDVSLEIQDLRLEDYGRYRCEVIDGLEDESGLVELELRGVVF PYQSPNGRYQFNFHEGQQ
VCAEQAAVVVASFEQLFRAWEELDWNCAGWLQDATVQYPIMLPRQPCGGPGLAPGVR SYGPR
HRRLHRYDVFCFATALKGRVYYLEHPEKLTLTEAREACQEDDATIAKVGQLFAAWKFHGLDR
CDAGWLADGSVRYPVVPVHPHPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

Signal sequence:

amino acids 1-17

Casein kinase II phosphorylation site.

amino acids 29-33, 53-57, 111-115, 278-282

Tyrosine kinase phosphorylation site.

amino acids 137-145

N-myristoylation site.

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

FIGURE 80

MMWRPSVLLLLLRLHGAQGKPSPDAGPHGQGRVHQAAPISDAPHDDAHGNFQYDHEAFLGR
EVAKEFDQLTPEESQARLGRIVDRMDRAGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDT
YDTDGRVGWEELRNATYGHYAPGEFFHDVEDAETYKKMLARDERRFRVADQDGDSMATRE
ELTAFLHPEEFPHMRDIVAETLEDLDRNKGYVQVEEYIADLYSAEPGEEEPAWVQTERQQ
FRDFRDLNKGHDGHLGSEVGHWVLPPAQDQPLVEANHLLHESDTDKDGRLSKAEILGNWNMFV
GSQATNYGEDLTRHHDEL

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 140-144

Casein kinase II phosphorylation site.

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,
291-295, 298-302

N-myristoylation site.

amino acids 263-269, 311-317

Endoplasmic reticulum targeting sequence.

amino acids 325-330

FIGURE 81

GGGGCCTGCCCTCCGCACTCGGGCGCAGCCGGTGGATCTCGAGCAGGTGGAGGCCCGG
GCGGCGGCGCGGGTGCAGGGATCCCTGACGCCTCTGTCCTGTTCTTGTGCTCCCAG
CCTGTCGTCGTCGTTGGCGCCCCCGCTCCCCCGCGGTGCGGGGTTGCACACCGATCCTG
GGCTCGCTCGATTGCCGCCAGGCGCCTCCAGACCTAGAGGGCGCTGGCCTGGAGCAG
CGGGCGTCTGTGTCCTCTCCTCTGCGCCGCCCGGGATCCGAAGGGTGCAGGGCTCT
GAGGAGGTGACGCGCGGGCCTCCGCACCCCTGCCCTGCCGCATTCTCCCTCTCCCAG
GTGTGAGCAGCCTATCAGTACCAATGTCCGCAGCCTGGATCCCAGCTCGGCCTCGGTGTG
TGTCTGCTGCTGCTGCCGGGCCGCGGGCAGCGAGGGAGCCCTCCATTGCTATCACATG
TTTACCAAGAGGCTTGACATCAGGAAAGAGAAAGCAGATGTCCTCTGCCAGGGGCTGCC
CTCTGAGGAATTCTCTGTGTATGGAACATAGTATATGCTCTGTATCGAGCATATGTGGG
GCTGCTGTCCACAGGGAGTAATCAGCAACTCAGGGGACCTGTACGAGTCTATAGCCTACC
TGGTCGAGAAAACATATTCTCAGTAGATGCCAATGGCATCCAGTCTCAAATGCTTCTAGAT
GGTCTGCTTCTTCACAGTAACAAAGGCAAAGTAGTACACAGGAGGCCACAGGACAAGCA
GTGTCACAGCACATCCACCAACAGTAAACGACTAAAGAAAACACCCGAGAAGAAAACCTGG
CAATAAAAGATTGAAAGCAGACATTGCAATTGATTGATGGAAGCTTAATATTGGCAGC
GCCGATTTAATTACAGAAGAATTGTGAAAGTGGCTCTAATGTTGGAATTGGAACA
GAAGGACCACATGTGGCCTTGTCAAGCCAGTGAACATCCAAAATAGAATTACTTGAA
AAACTTACATCAGCCAAAGATGTTTGTGCAATAAGGAAGTAGGTTTAGAGGGTA
ATTCCAATACAGGAAAAGCCTGAAAGCATACTGCTCAGAAATTCTCACGGTAGATGCTGGA
GTAAGAAAAGGGATCCCCAAAGTGGTGGTATTATTGATGTTGGCCTCTGATGACAT
CGAGGAAGCAGGCATTGTGGCCAGAGAGTTGGTGTCAATGTATTATAGTTCTGTGGCCA
AGCCTATCCCTGAAGAACTGGGATGGTCAGGATGTCACATTGTTGACAAGGCTGCTGT
CGGAATAATGGCTTCTCTTACACATGCCAACTGGTTGGCACCACAAAATACGTAAA
GCCTCTGGTACAGAAGCTGTGCACTCATGAACAAATGATGTGCAAGACCTGTTATAACT
CAGTGAACATTGCTTCTAATTGATGGCTCCAGCAGTGGAGATAGCAATTCCGCCTC
ATGCTGAATTGTTCCAACATAGCCAAGACTTTGAAATCTGGACATTGGTGCAGAT
AGCTGCTGTACAGTTACTTATGATCAGCGCACGGAGTTCACTGACTATAGCACCA
AAGAGAATGTCTAGCTGTCACTAGAAACATCCGCTATATGAGTGGAGACAGCTACTGGT
GATGCCATTCTTCACTGTTAGAAATGTGTTGGCCCTATAAGGGAGAGCCCCAACAGAA
CTTCTAGTAATTGTCACAGATGGCAGTCCTATGATGATGTCAGGCTTGGCAGCTGCTG
CACATGATGCAGGAATCACTATCTCTGTGTTGGCTGGCACCTCTGGATGACCTG
AAAGATATGGCTCTAAACGAAGGAGTCTCACGCTTCTCACAAGAGAGTTCACAGGATT
AGAACCAATTGTTCTGATGTCATCAGAGGCATTGTTAGAGATTCTTAGAATCCCAGCAAAT
AATGGTAACATTGACAACAGAAAGAAAAAGTACAAGGGATCCAGTGTGAAATTGTATT
CTCATAATACTGAAATGCTTACTGACATACTAGAACATCAGATACAAAATTAAGTATGTCAAC
AGCCATTAGGCAAATAAGCACTCCTTAAAGCCGCTGCCCTCTGGTTACAATTACAGTGT
ACTTTGTTAAAACACTGCTGAGGCTTCATAATCATGGCTCTAGAAACTCAGGAAAGAGGA
GATAATGTGGATTAAAACCTTAAGAGTTCAACCAGCCTACTAAATGTACAGATATGCAAA
TTCCATAGCTCAATAAAAGAACATGATACTTAGACCAAAAAAA

FIGURE 82

MSAAWI PALGLGVCLLLLPGPAGSEGA APIA ITCFTRGLDIRKE KADVLCPGGC PLEEF SVY
GNIVYASVSSICGAAVHRGVISNSGGPVRVYSLPGRENYSSVDANGIQSQMLSRWSASFTVT
KGKSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDC KADIAFLIDGSFNIGQRRFNLQKN
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLNFTSAKDVLFAI KEVGFRGGNSNTGKAL
KHTAQKFFTVDAGVRKGIPKVVVFIDGWP SDDIEEAGIVAREFGVN VFIVSVA KPIPEELG
MVQDVT FVDKAVCRNNNGFFSYHMPNWF GTTKYVKPLVQKLCTHEQMMCSKTCYNSVNIAFLI
DGSSSVGDSNFRLMLEFVSNIAKT FEIS DIGAKIAAVQFTYDQRTEFSFTDYSTKENV LAVI
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDG QSYDDVQGPAAAHDAGITI
FSVGVAWAPLDDLKDMASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

Signal sequence:

amino acids 1-24

N-glycosylation site.

amino acids 100-104, 221-225

Casein kinase II phosphorylation site.

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,
425-429, 478-482, 528-532

N-myristoylation site.

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

Amidation site.

amino acids 145-149

FIGURE 83

CGCCCGGCTCCGCACCCGGGGCCACCGCGCCGCTCCGCATCTGCACCCGAGCCC
GGCGGCCTCCGGGGAGCGAGCAGATCCAGTCCGGCCCGCAGCGCAACTCGGTCCAGTCG
GGCGGGCGGCTCGGGCGCAGAGCGGAGAT**TG**CAGCGGCTGGGCCACCTGCTGCGCTGC
TGCTGGCGGGCGGTCCCCACGGCCCCGCGCCGCTCCGACGGGACCTCGGCTCCAGTC
AAGCCGGCCGGCTCTCAGCTACCCGAGGAGGAGGCCACCTCAATGAGATGTTCCGCGA
GGTTGAGGAAGTGTGCTAAAGCATCATCAGAAGTGAACCTGGCAAACCTAACCTCCAGCTAT
CACAATGAGACCAACACAGACACGAAGGTTGAAATAATACCATCCATGTGCACCGAGAAAT
TCACAAGATAACCAACAAACCAGACTGGACAAATGGTCTTTAGAGACAGTTATCACATCTG
TGGGAGACGAAGAAGGAGCCACGAGTGCATCATCGACGAGGACTGTGGGCCAGC
ATGTAAGTGCAGTTGCCAGCTCCAGTACACCTGCCAGCCATGCCGGGGCAGAGGATGCT
CTGCACCCGGGACAGTGAGTGTGGAGACCAGCTGTGTCTGGGTCACTGCACCAAAA
TGGCCACCAGGGGAGCAATGGGACCATCTGTGACAACCAACAGAGGACTGCCAGCCGGGCTG
TGCTGTGCCTTCCAGAGAGGCTGCTGTTCCCTGTGACACCCCTGCCGTGGAGGGCGA
GCTTGCCATGACCCGCCAGCCGGCTCTGGACCTCATCACCTGGAGCTAGAGCCTGATG
GAGCCTTGGACCGATGCCCTGTGCCAGTGGCCTCTGGAGCTGCCAGCCCCACAGCCACAGCCTG
GTGTATGTGTGCAAGCCGACCTCGTGGGGAGCCGTGACCAAGATGGGAGATCCTGCTGCC
CAGAGAGGTCCCCGATGAGTATGAAGTTGGCAGCTCATGGAGGAGGTGCCAGGAGCTGG
AGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCGCTGGGGAGCCTGCCGGCTGCCGGCT
GCACTGCTGGGAGGGAAAGAGATT**TAG**ATCTGGACCAAGGCTGTGGTAGATGTGCAATAGAA
ATAGCTAATTATTCCCCAGGTGTGCTTAGGCGTGGCTGACCGAGGCTTCTTCTAC
TCTTCTTCCCAGTAAGTTCCCTCTGGCTTGACAGCATGAGGTGTTGTGCATTGTCAGC
TCCCCCAGGCTGTTCTCCAGGCTTCACAGTCTGGCTTGGAGAGTCAGGAGGGTAAAC
TGCAGGAGCAGTTGCCACCCCTGTCCAGATTATGGCTGCTTGCCTCTACCAGTTGGCAG
ACAGCCGTTGTTCTACATGGCTTGATAATTGTTGAGGGAGGAGATGGAACAAATGTGG
AGTCTCCCTCTGATTGGTTTGGGAAATGTGGAGAAGAGTGCCTGCTTGCAAACATCAA
CCTGGAAAAATGCAACAAATGAATTTCACGCAGTTCTTCCATGGCATAGGTAAGCTG
TGCCTTCAGCTGTTGCAGATGAAATGTTCTGTTCACCTGCATTACATGTGTTATTGATCC
AGCAGTGTGCTCAGCTCCTACCTCTGTGCCAGGGCAGCATTTCATATCCAAGATCAATT
CCTCTCTCAGCACAGCCTGGGAGGGGTATTGTTCTCCTCGTCCATCAGGGATCTCAGAG
GCTCAGAGACTGCAAGCTGCTGCCAAGTCACACAGCTAGTGAAGACCAGAGCAGTTCAT
CTGGTTGTGACTCTAACGCTCAGTGCTCTCCACTACCCACACCAGCCTGGTGCACCAA
AAAGTGTCCCCAAAAGGAAGGAGAATGGGATTTCTTGAGGCATGCACATCTGGAATTAAG
GTCAAACATAATTCTCACATCCCTCTAAAGTAAACTACTGTTAGGAACAGCAGTGTCTCAC
AGTGTGGGGCAGCCGTCTTCTAATGAAGACAATGATATTGACACTGTCCCTTTGGCAGT
TGCATTAGTAACATTGAAAGGTATATGACTGAGCGTAGCATACAGGTTAACCTGCAGAAACA
GTACTTAGGTAATTGTAGGGCGAGGATTATAAATGAAATTGCAAATCACTTAGCAGCAAC
TGAAGACAATTATCAACCACGTGGAGAAAATCAAACCGAGCAGGGCTGTGAAACATGGTT
GTAATATGCGACTGCGAACACTGAACCTACGCCACTCCACAAATGATGTTTCAGGTGTCA
TGGACTGTTGCCACCATGTATTGATCCAGAGTTCTTAAAGTTAAAGTGCACATGATTGTA
TAAGCATGCTTCTTGAGTTAAATTATGTATAAACATAAGTGCATTAGAAATCAAGC
ATAAAATCACTCAACTGCAAAAAAAAAAAAAAA

FIGURE 84

MQRLGATLLCLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQ
HKLRSAVEEMEAEEAAKASSEVNLPPSYHNETNTDKVGNNTIHVHREIHKITNNQTG
QMVFSETVITSVGDEEGRSHECIIDEDCGPSMYCQFASFQYTCQPCRQMLCTRSECCG
DQLCVWGHCTKMATRGSGNTICDNQRDCQPGGLCCAFQRGLFPVCTPLPVEGELCHDPASRL
LDLITWELEPDGALDRCPCASGLLCQPHSHSLVYVCKPTFVGSRDQDGIELLPREVPEYEV
GSFMEEVRQELEDLERSLTEEMALGEPAAAAALLGEEI

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 96-100, 106-110, 121-125, 204-208

Casein kinase II phosphorylation site.

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,
327-331

N-myristoylation site.

amino acids 202-208, 217-223

Amidation site.

amino acids 140-144

FIGURE 85

AAGGAGGGCTGGGAGGAAGAGGTAAGAAAGGTTAGAGAACCTACCTCACATCTCTGGGCTCAGAAGGACTCTG
AAGATAACAATAATTTCAGCCCATCCACTCTCCTTCCCTCCAAACACACATGTGCATGTACACACACACATACA
CACACATACACCTTCTCTCCACTGAAGACTCACAGTCACTCACTCTGTGAGCAGGTCATAGAAAAGGACAC
TAAAGCCTTAAGGACAGGCCATTACCTCTGCAGCTCTGGCTTGTGAGTCAAAAACATGGGAGGG
CCAGGCACGGTGAECTCACACCTGTAATCCCAGCATTTGGGAGACCGAGGTGAGCAGATCACTTGAGGTAGGG
TTCGAGACCAGCTGGCCAACATGGAGAAACCCCCATCTACTAAAAACAAAAATTAGCCAGGAGTGGTGGC
AGGTGCCTGTAATCCCAGCTACTCAGGTGGCTGAGCCAGGAGATCGCTGAATCCAGGAGGCGGAGGATGCAGT
CAGCTGAGTGCACCGCTGCACTCCAGCCTGGGTGACAGAATGAGACTCTGTCTAAACAAACAAACACGGGAGGA
GGGGTAGATACTGCTTCTGCAACCTCTTAACCTGCATCCTCTTCCAGGGCTGCCCTGATGGGCCCTG
GCAATGACTGAGCAGGCCAGGCCAGAGGACAAGGAAGGATATTGAGGAGGGCAAGAAGTGA
GCCCCG
GTGAGAATGACTGCCCTGGGAGGGTGGTCTTGGGCCCTGGCAGGGTGTGACCCCTTACCTGCAA
AACACA
AAGAGCAGGACTCCAGACTCTCTTGTAATGGTCCCCCTGCCAGCTCCACCATGAGGCTTCTCGTGGCCCC
ACTCTGCTAGCTTGGGTGGCTGGCAGTGCCTGTTGACCTGTCCTGGCTGGTACCCCTGGCATGTTCCCTGCC
GTGCTGCTGCCAGATCCGGGCTGGTATAACGCCCGCTCGTCTTACCGCCAGGCTACCAACTGIGGACTGCAATGA
CCTATTCTGACGGCAGTCCCCCGGACTCCCCCGGACAGAGGACCTGCTCTGCCAGAGCAACAGCATTGT
CCGTGTGGACAGAGTGA
GGCTGGCTACCTGGGCTACCTGGGCTACCTGGGCTACCTGGGCTACCTGGGCTACCTGGGCTACCTGGGCT
TGCCCGAGACTGTGATTTCATGCCCTGCCAGCTGCTGAGCCTGACCTAGAGGAGAACAGCTGACCCGGCT
GGAGGACACAGCTTGAGGGCTGGCAGGCCACAGGAACCTCTATCTAACCCACAAACAGCTAACCGCATCGC
CCCCAGGGCTTTCTGGCCTCAGCAACTTGCTGCCAGCTACAGGAACCTCTATCTAACCCACCTCTGAGGGCATTGACAG
CCGCTGGTTGAAATGCTGCCAACCTGCGTAGCCTGGTGTAGCAGGCTAGAACCTGCCGGAGATCTCGACTATGC
GAACCTCCGGCCCTGGCAACCTGCGTAGCCTGGTGTAGCAGGCTAGAACCTGCCGGAGATCTCGACTATGC
CCTGGAGGGCTGCAAAGCCTGGAGAGCCTCTCTATGACAACAGCTGCCGGGTGCCAGCGGGCACT
GGAACAGGTGCCGGCTCAAGTTCTAGACCTCAACAAGAACCCGCTCCAGCGGGTAGGGCCGGGGACTTGC
CAACATGCTGCACCTTAAGGAGCTGGACTGAACAAACATGGAGGAGCTGGTCTCATCGACAAGTTGCCCTGGT
GAACCTCCCCGAGCTGACCAAGCTGGACATACCAATAACCCACGGCTGCTTCTATCCACCCCCCGCGCCTTCCA
CCACCTGCCAGATGGAGACCCCTATGCTCAACAAACAGCTCTCAGTGCCTGCCAGCAGACGGTGGAGTC
CCTGCCAACCTGCAAGGAGGTAGGTCTCACGGCAACCCATCCGCTGTGACTGTGTCATCCGCTGGCCAATGC
CACGGCACCCGTGTCCGCTTCATCGAGCGCAATCCACCCGTGTGCGGAGCCTCCAGCGCCTCCCC
GGTCCGTGAGGTGCCCTCCGGGAGATGACGGACCACTGTTGCCCTCATCTCCCCACGAAGCTTCCCCCAAG
CCTCCAGGTAGCAGTGGAGAGAGCATGGTGTGCAATTGCCGGCACTGCCGAACCCGAACCGAGATCTACTG
GGTCACTCCAGTGGCTTCGACTGACACCTGCCATGCAGGCAGGAGGTACCGGGTGTACCCGAGGGACCC
GGAGCTGCGGAGGGTGACACAGAGGAGGCCAGGGTATACACCTGTGTTGGCCAGAACCTGGTGGGGCTGACAC
TAAGACGGTTAGTGTGGTTGTGGGCCGTCTCTCCAGCGAGGGAGCAAGGAGCAGGGCTGGAGCTCC
GGTGCAGGAGACCCACCCCTATCACATCCTGCTATCTGGGTCAACCCACACAGTGTCCACCAACCTCAC
CTGGTCCAGTGCTCCTCCCTCCGGGCCAGGGGCCACAGCTCTGGCCCTGCCCTGGGAAACCCACAGCTA
CAACATTACCCGCCCTTCAGGCCACGGAGTACTGGCCTGCCAGTGGCTGCAAGTGGCTTGTGATGCCACACCA
GTTGGCTGTGATGGGCCAGGACCAAAGAGGCCACCTCTGCCACAGAGCCTTAGGGATGTCCTGGCTCAT
TGCCATCCTGGCTCTGCTGCCCTCTGGCAGCTGGCTAGCGGCCACCTGGCACAGGCCACCCAGGAA
GGGTGTGGGTGGAGGGCGGCCCTCCGGCTGCCAGCTGGCTTCTGGGCTGGAGTGCCCTTCTGTCCGGTTGT
GTCTGCTCCCTCGTCCCTGCCCTGGAAATCCAGGGAGGAAGCTGCCAGATCCTCAGAAGGGAGACACTGTTGCC
ACCATTGTCTAAACATTCTTGAAGCTCAGCCTGTTCTCAGCAGTAGAGAAATCACTAGGACTACTTTTACCAA
AGAGAACAGTCTGGGCCAGATGCCCTGCCAGGAAAGGGACATGGACCCACGTGCTTGAGGCCAGCTGGC
CAAGACAGATGGGCTTGTGGCCCTGGGGTGTCTGCCAGCTGGCTGAGCCTTGTGAGGAGGCACTCCATCTC
CCTCTGCTGCCAGAGGCTCTGGCCTGGCTTGTCTGCCCTACCTGTGTCCTCCGGCTGCCACCCCTCTCT
TCTTCTCTGTACAGTCTCAGTTGCTTGTGCTCTTGCTGCCCTGGCAAGGGCTGAAGGAGGCCACTCCATCTC
CTCGGGGGCTGCCCTCAATGTGGAGTGACCCAGCCAGATCTGAAGGACATTGGAGAGGGATGCCAGGAA
CGCCTCATCTCAGCAGCCTGGCTGCCATTCCGAAGCTGACTTCTATAGGCAATTGTACCTTGTGGAGAA
ATGTGTACACCTCCCCAACCCGATTCACTCTTCTCTGTGTTGAAAAATAAAATAAAACAATAAAA
AAAA

FIGURE 86

MRLLVAPLLLAWVAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFLTA
VPPALPAGTQTLLLQSNSIVRVDQSELGYLANLTELDLSQNSFSDARDCDFHALPQLLSLHL
EENQLTRLEDHSFAGLASLQEYLHNQLYRIAPRAFSGLSNLLRLHLSNLLRAIDSRWFE
MLPNLEILMIGGNKVDAILDMNFRPLANLRSVLVLAGMNLRREISDYALEGLQSLESLSFYDNQ
LARVPRRALEQVPGLKFLDLNKPLQRVPGDFANMLHLKELGLNNMEELVSIDKFALVNLP
ELTKLDITNNPRLSFIHPRAFHHLQPQMELMLNNNALSALHQQTVESLPNLQEVGLHGNPIR
CDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPFREMTHCLPLISPRSFPPSLQ
VASGESMVLHCRALAEPEPEIYWVTPAGLRLTPAHAGRRYRVYPEGTLELRRVTAAEAGLYT
CVAQNLVGADTKTVSVVGRALLQPGRDEGQGLELRVQETHPYHILLSWVTPPNTVSTNLTW
SSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVAFADAHTQLACVWARTKEATS
CHRALGDRPGLIAILALAVALLLAAGLAHLGTGQPRKGVGGRRPLPPAWAFWGWSAPSVRVV
SAPLVLPWNPGRKLPRSSGETLLPPLSQNS

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 629-648

N-glycosylation site.

amino acids 94-98, 381-385, 555-559, 583-587

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 485-489

Casein kinase II phosphorylation site.

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,
243-247, 313-317, 488-492, 700-704

Tyrosine kinase phosphorylation site.

amino acids 532-540

N-myristoylation site.

amino acids 15-21, 493-499, 566-572

Amidation site.

amino acids 470-474, 660-664, 692-696

FIGURE 87

FIGURE 88

MRQTIIKVIKFILIICTVYYVHNIKFVDVDC TVDIESLTGYRTYRCAHPLATLFKILASFYI
SLVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSK
RFAVFLSEVSENKLRLQLNNEWTLDKLQRQLTKNAQDKLELHLFMLS GIPDTVFDLVELEV
LKLELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPAL AFLRENLRALHIKFDTIKEIPLWI
YSLKTLEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKS NLSKLPQVVTDVGVHLQKLSI
NNEGTKLIVLNSLKKMANLTEL ELIRCDLERIPH SIFSLHNLQEIDLKDNNLKTIEEIISFQ
HLHRLTCLKLWYNHIAYIPIQIGNLTNERLYLNRNKIEKIPTQLFYCRKLRYLDLSHNNLT
FLPADIGLLQNLQNLAITANRIETLPPPELFQCRKLRALHLGNNVLQSLPSRVGE LTNL TQIE
LRGNRLECLPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

Transmembrane domain:

amino acids 51-75 (type II)

N-glycosylation site.

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 85-89

Casein kinase II phosphorylation site.

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,
398-402, 493-497

N-myristoylation site.

amino acids 173-179, 261-267, 395-401, 441-447

FIGURE 89

GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGCGCTCTCCCGT
CCCGCGGTGGTTGCTGCTGCCGTGCTGGCCTGAACGCAGGAGCTGTCAATTGACT
GGCCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATG
TTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCTGGTCAT
GTGGCTTCAGGGCGGTCCAGGCAGGTTCTAGCACTGGATTGGAAACTTGAGGAAATTGGC
CCCTTGACAGTGTACTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCCAGTCTCCTATT
GTGGATAATCCCCTGGGACTGGGTTCAAGTGTGAATGGTAGTGGTGCCTATGCCAAGGA
CCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGAACCTTCTCAGTTGCCACAAAG
AATTCCAGACAGTTCCATTCTACATTTCTCAGAGTCCTATGGAGGAAAATGGCAGCTGGC
ATTGGTCTAGAGCTTATAAGGCCATTAGCGAGGGACCATCAAGTGCACCTTGCGGGGGT
TGCCTGGGTGATTCCCTGGATCTCCCTGTTGATTGGTCTCCTGGGACCTTACCTGT
ACAGCATGTCTCTCGAAGACAAAGGTCTGGCAGAGGTGTCAAGGTTGCAGAGCAAGTA
CTGAATGCCGTAATAAGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGAAAGCAGAAAT
GATCATTGAACAGAACACAGATGGGTGAACCTCTATAACATCTTAACACTAAAGCACTCCA
CGTCTACAATGGAGTCGAGTCTAGAATTACACACAGAGGCCACCTAGTTGTCTTGTAGCGC
CACGTGAGACACCTACAACGAGATGCCTTAAGCCAGCTCATGAATGGCCCCATCAGAAAGAA
GCTAAAATTATTCCCTGAGGATCAATCCTGGGAGGCCAGGCTACCAACGTCTTGTGAACA
TGGAGGAGGACTTCATGAAGCCAGTCATTGACATTGTGGACGAGTTGCTGGAGGCAGGGATC
AACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATAACCAGGGTCAGGAGGCCTG
GGTGGAAACTGAAGTGGCCAGAACTGCCTAAATTCAAGTCAGCTGAAGTGGAAAGGCCCTGT
ACAGTGACCCCTAAATCTTGGAAACATCTGCTTTGTCAAGTCCTACAAGAACCTTGCTTT
TACTGGATTCTGAAAGCTGGTCATATGGTTCTCTGACCAAGGGACATGGCTCTGAAGAT
GATGAGACTGGTGA~~C~~CAAGAATGGATGGCTGGCTGTTGGCT
TGGGGCACAGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGGCCATTCTCCCTGTATCT
AACTGGGCTGTGATCAAGAAGGTTCTGACCAGCTCTGCAGAGGATAAAATCATTGTCTCT
GGAGGCAATTGGAAATTATTCTGCTCTTAAAAAAACCTAAGATTTTAAAAAATTGAT
TTGTTTGATCAAAATAAGGATGATAATAGATATTAA

FIGURE 90

MELALRRSPVPRWLLLPLLLGLNAGAVIDWPTEEGKEWWDYVTVRKDAYMFWWLYYATNSC
KNFSELPLVMWLQGGPGGSSTGFGNFEIGPLSDLKPRKTTWLQAASLLFVDNPVGTGFSY
VNGSGAYAKDLAMVASDMMVLLKTFFSCHKEQTVPFYIFSESYGGKMAAGIGLELYKAIQR
GTIKCNFAGVALGDSWISPDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNAVNKGLYRE
ATELGKAEMIIEQNTDGVNFYNILTKSTPTSTMESLEFTQSHLVCLCQRHVRHLQRDALS
QLMNGPIRKKLKIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQLDL
IVDTMGQEAWVRKLKWPELPKFSQLWKALYSDPKSLETSAFVKSYKNLAFYWILKAGHMVP
SDQGDMALKMMRLVTQQE

Signal sequence:

amino acids 1-25

N-glycosylation site.

amino acids 64-68, 126-130, 362-366

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 101-105

Casein kinase II phosphorylation site.

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

N-myristoylation site.

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,
187-193, 195-201, 331-337, 332-338, 360-366

FIGURE 91

GGCCGCGGGAGAGGAGGCCATGGCGCGCGCGCGCTGCTGCTGGCGCTGCTGCTGGCTC
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCCGCGCTTATCAGGACCATGCGCCGA
CGGGTCATCACGTGCGCATCGTGGGTGGAGAGGACGCCACTCGGGCGTGGCCGTGGCA
GGGGAGCCTGCGCCTGTGGATTCCCACGTATGCGGAGTGAGCCTGCTCAGCCACCCTGGG
CACTCACGGCGGCGCACTGCTTGAAACCTATAGTGACCTTAGTGATCCCTCCGGTGGATG
GTCCAGTTGGCCAGCTGACTTCCATGCCATCCTCTGGAGCCTGCAGGCCACTACACCCG
TTACTTCGTATCGAATATCTATCTGAGCCCTCGTACCTGGGAATTCACCTATGACATTG
CCTTGGTGAAGCTGTCTGCACCTGTACCTACACTAAACACATCCAGCCCACCTGTCTCCAG
GCCTCCACATTGAGTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGTACATCAA
AGAGGATGAGGCACTGCCATCCCCACACCCTCCAGGAAGTTCAGGTGCCATATAAACAA
ACTCTATGTGCAACCACCTCTCCTCAAGTACAGTTCCGCAAGGACATCTTGGAGACATG
GTTTGTGCTGGCAACGCCAACGGGGAGGATGCCTGCTCGGTGACTCAGGTGGACCCTT
GGCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGAGTGGCTGTG
GTCGCCCAATCGGCCGGTGTACACCAATATCAGCCACCCTTGAGTGGATCCAGAAG
CTGATGGCCCAAGACTGGCATGTCCCAGCCAGACCCCTCTGGCCACTACTCTTTCCCTCT
TCTCTGGCTCTCCACTCCTGGGCCGGTCTTGAGCCTACCTGAGCCCATGCAGCCTGGGG
CACTGCCAAGTCAGGCCCTGGTCTCTGTCTTGGTAATAAACACATTCCAGTTGA
TGCCTTGCAGGGCATTCTCAAAAAAAAAAAAAAAA

FIGURE 92

MGARGALLALLLARAGLRKPEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSLRLW
DSHVCVSSLHRWALTAACFETYSDLSDPGWMQFGQLTSMPSFWSLQAYYTRYFVSNI
YLSPTYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALP
SPHTLQEVAIIINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDSGGPLACNKNG
LWYQIGVVSWGVGCGRPVRPGVYTNIHHFEWIQKLMAQSGMSQPDPSWPLLFFPLLWALPL
LGPV

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 167-171, 200-204, 273-277

Casein kinase II phosphorylation site.

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

N-myristoylation site.

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,
259-265, 269-275

Amidation site.

amino acids 33-37

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 252-263,

Serine proteases, trypsin family, histidine active site.

amino acids 78-84

FIGURE 93

CCACCGCGTCCGGAGCGGTGGGAAGGGAGAATGGACTCCAAGCCTGCCTCTAGGGCT
CTTGCCCTCATCCTCTGGCAAATGCAGTTACAGCCGGAGCCCCGACCAGCGGAGGACGC
TGCCCCCAGGCTGGGTGCCCTGGGCCGTGCGGACCTGAGGAAGAGCTGAGTCTCACCTT
GCCCTGAGACAGCAGAAATGTGGAAAAGACTCTCGGAGCTGGTGCAGGCTGTGTCGGATCCCAG
CTCTCCTCAATACGGAAAATACCTGACCCTAGAGAATGTGGCTATCGGTGAGGCCATCCC
CACTGACCCCTCCACACGGTGCAAAAATGGCTCTTGGCAGCCGGAGCCAGAAGTGCCATTCT
GTGATCACACAGGACTTCTGACTTGCTGGCTGAGCATTCCGACAAGCAGAGCTGCTGCTCCC
TGGGGCTGAGTTCATCACTATGTGGAGGACCTACGGAAACCCATGTTGAAGGTCCCCAC
ATCCCTACCAGCTCCACAGGCCTGGCCCCCATGTGGACTTGTGGGGGACTGCACCGT
TTTCCCCCAACATCATCCCTGAGGCAACGTCTGAGCCGCAGGTGACAGGGACTGTAGGCCT
GCATCTGGGGTAACCCCTCTGTGATCCGTAAAGCATACTTGACCTCACAAAGACGTGG
GCTCTGGCACCAGCAATAACAGCCAAGCCTGTGCCAGTTCTGGAGCAGTATTCCATGAC
TCAGACCTGGCTCAGTTCATGCCCTTCCGGTGGCAACTTGACATCAGGCATCAGTAGC
CCGTGTGGTTGACAACAGGGGGGGGGGGGGGGATTGAGGCCAGTCTAGATGTGCAGT
ACCTGATGAGTGGTGCACACATCTCCACCTGGGTCTACAGTAGGCCCTGGCCGGCATGAG
GGACAGGAGCCCTCCTGCAGTGGCTCATGCTCAGTAATGAGTCAGCCCTGCCACATGT
GCATACTGTGAGCTATGGAGATGAGGACTCCCTCAGCAGGCCACATCAGCGGGTCA
ACACTGAGCTCATGAAGGCTGCCGCTGGGGTCTACCCTGCTTCTGCCTCAGGTGACAGT
GGGGCCGGGTGTTGGTCTGTCTCTGGAAAGACACCAGTCCGCCCTACCTTCCCTGCCTCCAG
CCCCTATGTCACCACAGTGGGAGGCACATCCTCAGGAACCTTCCATCACAAATGAAA
TTGTTGACTATATCAGTGGTGGCTTCAGCAATGTGTTCCCACGGCCTCATACCAGGAG
GAAGCTGTAACGAAGTCTGAGCTTAGCCCCCACCTGCCACCATCCAGTTACTTCATG
CAGTGGCCGTGCCCTACCCAGATGTGGCTGCACTTCTGATGGCTACTGGGTGGTCAGCAACA
GAGTGCCCATCCATGGGTGTCGGAACCTCGGCCCTACTCCAGTGTGTTGGGGGATCCTA
TCCTTGATCAATGAGCACAGGATCCTTAGTGGCCCCCCCTCTGGCTTCTCAACCCAAG
GCTCTACCAGCAGCATGGGGCAGGTCTTTGATGTAACCCGTGGCTGCCATGAGTCCTGTC
TGGATGAAGAGGTAGAGGGCCAGGGTTCTGCTCTGGCTGGGATCCTGTAACAGGC
GGGGAAACACCAACTTCCAGCTTGCTAAGACTCTACTCAACCCCTGACCCTTCTATC
AGGAGAGATGGCTTGTCCCTGCCCTGAAGCTGGCAGTTCACTGCCCTATTCTGCCCTGTTG
GAAGCCCTGCTGAACCCCTCAACTATTGACTGCTGCAGACAGCTTATCTCCCTAACCCCTGAAA
TGCTGTGAGCTGACTTGACTCCCAACCCCTACCATGCTCCATCATACTCAGGTCTCCCTACT
CCTGCCCTAGATTCCCTCAATAAGATGCTGTAACTAGCATTGGATGCCCTCTCCCTCCGC
ATCTCATCTTCTTTCAATCAGGCTTCCAAAGGGTTGTATACAGACTCTGTGCACTA
TTTCACTTGATATTCAATTCCCCAATTCACTGCAAGGAGACCTCTACTGTCACCCTTACTCT
TTCCTACCCCTGACATCCAGAAACAAATGGCCTCCAGTGCATACTTCTCAATCTTGTGTTATG
GCCTTCCATCATAGTTGCCACTCCCTCCTACTTAGCTTCCAGGTCTTAACCTCTG
ACTACTCTTGCTTCCCTCTCATCAATTCTGCTTCTCATGGAATGCTGACCTCATTGC
TCCATTGAGATTGGCTTCTCAGTTACTCATTGTCCCTGGAACAAATCACTGACA
TCTACAACCATTACCATCTCACTAAATAAGACTTCTATCCAATAATGATTGATACTCTAAA
TGTAAAAAA

FIGURE 94

MGLQACLLGLFALILSGKCSYSPEPDQRRTLPPGVSLGRADPEEELSLTFALRQQNVERLS
ELVQAVSDPSSPQYGYLTLENVALVRPSPLTLHTVQKWLLAAGAQKCHSVITQDFLTCWL
SIRQAELLPGAEFHYYVGGPTETHVVRSPHPYQLPQALAPHVDFVGGHLRFPPSSLRQRP
EPQVTGTVGLHLGVTPSVIRKRYNLTSQDVGSCTSNNSQACAQFLEQYFHDSDLAQFMRLFG
GNFAHQASVARVVGQQGRGRAGIEASLDVQYLMSAGANISTWVYSSPGRHEGQEPFLQWLML
LSNESALPHVHTVSYGDDEDSLSSAYIQRVNTELMKAARGLTLLFASGDGAGCWSVSGRH
QFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGGFSNVFPRPSYQEEAVTKFLSSSP
HLPPSSYFNASGRAYPDVAALSDGYWVVSNRVPIPWVSGTSASTPVFGGILSLINEHRILSG
RPPLGFLNPRLYQQHGAGLFDVTRGCHESCLDDEVEGQGFCSGPWDPVTGWGTPTSQLC

Signal sequence:

amino acids 1-16

N-glycosylation site.

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

Glycosaminoglycan attachment site.

amino acids 361-365, 408-412, 538-542

Casein kinase II phosphorylation site.

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

N-myristoylation site.

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,
521-527, 533-539, 549-555

FIGURE 95

GCCGCGCGCTCTCCGGGCCACACCTGTCTGAGCGGCAGCGAGCCGGCCGGC
GGGCTGCTCGCGCGGAACAGTGCTCGGCATGGCAGGGATTCCAGGGCTCCTCTTCTC
TTCTTCTGCTCTGTGCTGTTGGCAAGTGAGCCCTACAGTGCCCCCTGGAAACCCACTTG
GCCTGCATAACCGCCTCCCTGTCGTCTTGCCCCAGTCTACCCCTAATTAGCCAAGCCAGACT
TTGGAGCCGAAGCAAATTAGAAGTATCTTCTTATGTGGACCCCAGTGTCTAAGGGAACT
CCACTGCCACTTACGAAGAGGCCAAGCAATATCTGTCTTATGAAACGCTCTATGCCAATGG
CAGCCGCACAGAGACGCAGGTGGCATCTACATCCTCAGCAGTAGTGGAGATGGGCCAAC
ACCGAGACTCAGGGTCTTCAGGAAAGTCTCGAAGGAAGCGGCAGATTATGGCTATGACAGC
AGGTTCAGCATTGGAGGACTTCCTGCTCAACTACCCTTCTCACAGCTGCCACTGCA
TACACGATGGAAAAACCTATGTGAAAGGAACCCAGAAGCTTCAGTGGCTTCTAAAGCCC
AAGTTAAAGATGGTGGCGAGGGGCCAACGACTCCACTTCAGCCATGCCGAGCAGATGAA
ATTCAGTGGATCCGGTGAAACGCACCCATGTGCCCAAGGGTTGGATCAAGGGCAATGCCA
ATGACATCGGCATGGATTATGATTATGCCCTCTGGAACTCAAAAGCCCCACAAGAGAAAA
TTTATGAAGATTGGGTGAGCCCTCTGCTAAGCAGCTGCCAGGGGCAGAATTCACTTCTC
TGGTTATGACAATGACCGACCAGGCAATTGGTGTATCGCTCTGTGACGTCAAAGACGAGA
CCTATGACTTGCTCTACCAGCAATGCGATGCCAGCCAGGGCCAGCGGTCTGGGTCTAT
GTGAGGATGTGGAAGAGACAGCAGCAGAAGTGGAGCGAAAATTATTGGCATTTCAGG
GCACCACTGGTGGACATGAATTGCTTCCACAGGATTCAACGTGGCTGTCAAATCACTC
CTCTCAAATATGCCAGATTGCTATTGGATTAAAGGAAACTACCTGGATTGTAGGGAGGGG
TGAACACAGTGGTCCCTCTGGCAGCAATTAAAGGGCTTCTGTTCTTATTAGGAGAGGCC
AAATTGTTTTGTCTTGGCGTGCACACGTGTGTGTGTGTGTGTGTAAAGGTGT
CTTATAATCTTACCTATTCTTACAATTGCAAGATGACTGGCTTACTATTGAAAATCTG
GTTTGTGTATCATATCATATCATTAAGCAGTTGAAGGCATACTTTGCATAGAAATAA
AAAAAAACTGATTGGGCAATGAGGAATATTGACAATTAAAGTTAATCTCACGTTTGT
CAAACCTTGATTTATTCATCTGAACCTGGTTCAAAGATTATTAATTTAGGAGAGGCC
CAAGAGATATGAAAAAAAAAAAAAA

FIGURE 96

MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLHQSTLNLAQPDFGAEAKLEVS
SSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDGSQSGKS
RRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAACIHDGKTYVKG
TQKLRVGFLKPDKFDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNANDIGMDYDYA
LLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDETYDLQQCD
AQPGASGSGVYVRMWKRQQQWERKIIGIFSGHQWVDMNGSPQDFNVAVRITPLKYAQICYW
IKGNYLDCREG

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 93-97, 207-211

Glycosaminoglycan attachment site.

amino acids 109-113, 316-320

Casein kinase II phosphorylation site.

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

N-myristoylation site.

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

Serine proteases, trypsin family, histidine active site.

amino acids 171-177

FIGURE 97

GCATGCCCTGGGTCTCTCGAGCCTGCTGCCTGCTCCCCGCCCCACCAGCCATGGTGGTT
CTGGAGCGCCCCCAGCCCTGGGTGGGGCTGTCTCGGCACCTCACCTCCCTGCTGCTGCTG
GCGTCGACAGCCATCCTCAATGCGGCCAGGATAACCTGTTCCCCAGCCTGTGGGAAGCCCCA
GCAGCTGAACCGGGTTGTGGCGCGAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA
GCATCCAGAAGAATGGGACCCACCAGTGCAGGTTCTCTGCTCACCAAGCCGCTGGGTGATC
ACTGCTGCCACTGTTCAAGGACAACCTGAACAAACCATACCTGTTCTCTGCTGCTGGG
GGCCTGGCAGCTGGGAACCCCTGGCTCTCGGTCCCAGAAGGTGGGTGTTGCCTGGGTGGAGC
CCCACCCCTGTATTCTGGAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCGTCTCGAG
CGCTCCATACAGTTCTCAGAGCGGGCCTGCCATCTGCCTACCTGATGCCCTATCCACCT
CCCTCCAAACACCCACTGCTGGATCTCAGGCTGGGGAGCATCCAAGATGGAGTTCCCTTGC
CCCACCCCTCAGACCCTGCAGAACGCTGAAGGTTCTATCATCGACTCGGAAGTCTGCAGCCAT
CTGTACTGGCGGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGTGCCGGCTACTT
GGAGGGGGAGCGGGATGTTGCTGGCGACTCCGGGGCCCCCTCATGTGCCAGGTGGACG
GCGCCTGGCTGCTGGCGGCATCATCAGCTGGGCGAGGGCTGTGCCGAGCGCAACAGGCC
GGGGTCTACATCAGCCTCTCGCGCACCGCTCTGGTGAGAAGATCGTCAAGGGGTGCA
GCTCCCGGGCGCGCTCAGGGGGTGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGCCG
CCCGCGCTCCTAGGGCGCAGCGGGACGCAGGGCTCGGATCTGAAAGGCGGCCAGATCCACA
TCTGGATCTGGATCTCGGGCGGCCTCGGGCGTTCCCCCGCCGTAAATAGGCTCATCTACC
TCTACCTCTGGGGGCCGGACGGCTGCTGCGAAAGGAAACCCCTCCCCGACCGCCCCGAC
GGCCTCAGGCCCCCTCCAAGGCATCAGGCCGCCAACGGCCTCATGTCCCCGCCAC
GACTTCCGGCCCCGCCGGGGCCCCAGCGCTTTGTGTATATAATGTTAATGATTAT
AGGTATTTGTAACCTGCCACATATCTTATTATTCTCCAATTCAATAAATTATTATT
CTCCAAAAAAA

FIGURE 98

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318
><subunit 1 of 1, 317 aa, 1 stop
><MW: 33732, pI: 7.90, NX(S/T): 1
MVVSGAPPALGGGCLGTFTSLLLLASTAILNAARIPVPPACGKPQQLNRVVGGEDSTDSEWP
WIVSIQKNGTHHCAGSLLTSRWVITAACFKDNLNKPYLFSVLLGAWQLGNPGSRSQKVGVA
WVEPHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGWGSIQDG
VPLPHPQTLQKLKVPIIDSEVCSHLYWRGAGQGPITEDMLCAGYLEGERDACLGDGGPLMC
QVDGAWLLAGIIISWGEGCAERNRPGVYISLSAHRSWEKIVQGVQLRGRAQGGGALRAPSGQ
SGAAARS
```

Signal sequence:

amino acids 1-32

N-glycosylation site.

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 99

GACGGCTGCCACCATGCACGGCTCCTGCAGTTCTGATGCTTCTGCTGCCGCTACTGCTA
CTGCTGGTGGCCACCACAGGCCCCGTTGGAGCCCTCACAGATGAGGAAGACGTTGATGGT
GGAGCTGCACAACCTCTACCGGGCCCAGGTATCCCCGACGGCCTCAGACATGCTGCACATGA
GATGGGACGAGGAGCTGGCCGCCTCGCCAAGGCCTACGCACGGCAGTGCCTGTGGGCCAC
AACAAAGGAGCGCGGGCGCCGGCGAGAATCTGTCGCCATCACAGACGAGGGCATGGACGT
GCCGCTGGCCATGGAGGAGTGGCACCACGAGCGTGAGCACTACAACCTCAGGCCGCCACCT
GCAGCCCAGGCCAGATGTGCGGCCACTACACGCAGGTGGTATGGCCAAGACAGAGAGGATC
GGCTGTGGTTCCCACCTCTGTGAGAAGCTCCAGGGTGTGAGGAACCAACATCGAATTACT
GGTGTGCAACTATGAGCCTCCGGGAACGTGAAGGGAAACGCCCTACCAGGAGGGACTC
CGTGCTCCCAATGTCCCTCTGGCTACCACTGCAAGAACTCCCTCTGTGAACCCATCGGAAGC
CCGGAAGATGCTCAGGATTGCCTTACCTGGTAAC TGAGGCCCATCCTCCGGCGACTGA
AGCATCAGACTCTAGGAAAATGGGTACTCCTTCTTCCCTAGCAACGGGATTCCGGCTTCT
TGGTAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTCTGCCCTGCTGTGGAAACCCAGGCC
CCAACCTCCTTAGCAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCCACCTGCGTAAC
AACTGAGGTCCCTTCCATTTGGCAGCTCACAGCCTGCCCTCTGGATGAGGAGCCAGTTA
CCTTCCCCAAATCGACCCATGTTCCATCCAAAATCAGCAGACAAAGTGAACAGACAAAACA
AAAGTGCCCTCTAGGAGCCCAGAGAACTCTCTGGACCCCAAGATGTCCCTGACAGGGCAAG
GGAACCTCCTACCCATGCCAGGAGGAGGCTGAGGCTGAGGTGAGCTGCCCTCCAGTG
AGGTCTTGGCCTCAGTTTCCAGCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGAC
CACACGGGGCACACCTCCTCCAAGTCCCTGCCAATTCCCAATACCTCTGCCACCGCTAA
TGCCACGGGTGGCGTGCCTGGCTCTGCAGTCGCTGCCAGGTGCAGAGGCCCTGACA
AGCCTAGCGTTGTGTCAGGGCTGAACCTGGCCCTGGTCATGTGTGGGCCCTCTGGGA
CTACTGCTCCTGCCTCTGGTGTGGCTGGAATCTTCTGAATGGGATACCAACTCAAAGGG
TGAAGAGGTCAGCTGTCCTCTGTCACTTCCCCACCCCTGTCCCCAGGCCCTAAACAAGATA
CTTCTTGGTTAAGGCCCTCCGAAGGGAAAGGCTACGGGCATGTGCCCTCATCACACCATCC
ATCCTGGAGGCACAAGGCCTGGCTGGCTGCGAGCTCAGGAGGCCCTGAGGACTGCACACC
GGGCCACACCTCTCCCTGCCCTCCCTGAGTCCTGGGGTGGAGGATTGAGGGAGCT
CACTGCCTACCTGGCTGGGCTGTCTGCCACACAGCATGTGCCTCTCCCTGAGTCCTG
TGTAGCTGGGGATGGGGATTCCCTAGGGCAGATGAAGGACAAGCCCCACTGGAGTGGGGTTC
TTTGAGTGGGGAGGCAGGGACGAGGAAGTAACCTGACTCTCCAATAAAACCT
GTCCAACCTGTGAAA

FIGURE 100

MHGSCSFLMLLPLLLLVATTGPVGALTDEEKRLMVELHNLYRAQVSPTASDMLHMRWDEE
LAAFAKAYARQCVWGHNKERGRRGENLFAITDEGMVDPLAMEEWHHEREHYNLSAATCSPGQ
MCGHYTQVVWAKTERIGCGSHFCEKLQGVEETNIELLVCNYEPPGNVKGKRPYQEGETPCSQC
PSGYHCKNSLCEPIGSPEADAQDLPYLVTTEAPSFRATEASDSRKMGTPSSLATGIPAFLVTEV
SGSLATKALPAVETQAPTSLATKDPPSMATEAPPCVTTEVPSILAHSPLSLDEEPVTFPKS
THVPIPKSADKVTDKTKVPSRSPENSLDPKMSLTGARELLPHAQEEAEAAELPPSSEVLAS
VFPAQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSLPGAEGPDKPSVV
SGLNSGPGHVWGPLLGLLLLPLVLAGIF

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 114-118, 403-407, 409-413

Glycosaminoglycan attachment site.

amino acids 439-443

Casein kinase II phosphorylation site.

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

N-myristoylation site.

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,
250-256

Amidation site.

amino acids 82-86, 172-176

Peroxidases proximal heme-ligand signature.

amino acids 287-298

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.

amino acids 127-138

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.

amino acids 160-172

FIGURE 101

GTAAGTGAAGTCAGGCTTTCATTTGGGAAGCCCCCTCAACAGAATTGGTCATTCTCCAAGTTATGGTGGACGT
ACTTCTGTTGTTCTCCCTCTGCTTGCTTTCACATTAGCAGACCGGACTTAAGTCACAACAGATTATCTTTCAT
CAAGGCAGTTCCATGAGCCACCTTCAAAGCCTCGAGAAAGTGAACAAACAATGAATTGGAGACCATTCC
AAATCTGGGACCAAGTCTCGGCAAATATTACACTCTCTCCTGGCTGAAACAGGATTGTTGAAATACTCCCTGA
ACATCTGAAAGAGTTTCAGTCCCTTGAACATTGGACCTTAGCAGCAACAATATTTCAGAGCTCCAAACTGCATT
TCCAGCCCTACAGCTCAAATATCTGATCTCAACAGCAACCGAGTCACATCAATGGAACCTGGTATTTGACAA
TTTGGCCAACACACTCCTTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCCCACCCAAGATGTTAAACT
GCCCAACTGCAACATCTGAATTGAACCGAAACAAGATTAATAGTAGATGGACTGACATTCCAAGGCCTGG
TGCTCTGAAGTCTCTGAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTTGGGGCTGAGCAA
CATGAAATTTCAGCAGCTAACACACTAACAGAGATTACCAAAGGCTGGCTTACGGCTTGCTGATGCT
GCAGGAACCTCATCTCAGCAGGAAATGCCATCAACAGGATCAGCCCTGATGCCCTGGAGTTCTGCCAGAGCTCAG
TGAGCTGGACCTAACTTCAATCACTTCAAGGTTAGATGATTCAAGCTCCTGGCCTAAGCTTACTAAATAC
ACTGCACATTGGGAAACACAGAGTCAGCTACATTGCTGATTGTCCTCCGGGGCTTCCAGTTAAAGACTTT
GGATCTGAAGAACAAATGAAATTCTGGACTATTGAAGACATGAATGGCTTCTCTGGGCTTGACAAACTGAG
GCGACTGATACTCCAAGGAATCGGATCCGTTCTATTACTAAAAAGCCTTCACTGGTTGGATGCATTGGAGCA
TCTAGACCTGAGTGACAACGCAATCATGTTACAAGGCAATGCATTTCACAAATGAAGAAACTGCAACAATT
GCATTAAATACATCAAGCCTTGTGCGATTGCCAGCTAAATGGCTCCACAGTGGTGCGGAAAACAACCTT
TCAGAGCTTGTAAATGCCAGTTGTGCCATCCTCAGCTGCTAAAGGAAGAACGATTGGCTGTTAGCCAGA
TGGCTTGTGTTGATGATTTCCAAACCCAGATCACGGTTCAGGCCAGAAACACAGTCGCAATAAAAGGTT
CAATTGAGTTTCATCTGTCAGCTGCCAGCAGCAGTGATTCCCAATGACTTTGCTTGGAAAAAAAGACAATGA
ACTACTGCATGATGCTGAAATGGAAATTATGACACACCTCCGGGCCCCAAGGTGGCAGGGTGTGGAGTATACCAC
CATCCTCGGCTGCGAGGTGGAATTGCCAGTGAGGGAAATATCAGTGTGTCATCTCAATCATTGGTT
ATCCTACTCTGTCAAAGCCAAGCTTACAGTAAATATGCTTCCCTCATTCACCAAGACCCCCATGGATCTCACCAT
CCGAGCTGGGGCCATGGCACGCTGGAGTGCTGCTGTGGGGCACCCAGCCCCCAGATAGCCTGGCAGAGGA
TGGGGCACAGACTCCCGCTGCACGGAGAGACGCATGCTGATGCCAGGGATGACGTGTTCTTATCGT
GGATGTAAGAGATGAGACATTGGGTATACAGCTGCACAGCTCAGAACAGTGCAGGAAGTATTCAGCAAATGC
AACTCTGACTGTCCTAGAACACCATCATTTCAGGCCACTGTTGACCGAATGTAACCAAGGGAGAACAGC
CGTCCTACAGTGCAATTGCTGGAGGAAGCCCTCCCCCTAAACTGAACCTGGACCAAAGATGATAGCCATTGGTGG
AACCGAGAGGCACTTTTGCAAGCAGGCAATCAGCTCTGATTATTGTGGACTCAGATGTCAGTGTGCTGGGAA
ATACACATGTGAGATGTCACACACCCCTGGCACTGAGAGAGGAAACGTGCGCCTCAGTGTGATCCCCACTCCAAC
CTGCACTCCCCCTCAGATGACAGCCCCATGTTAGACGATGACGGATGGCCACTGTGGTGTGTCATAGC
CGTGGTTGCTGTGGGGCACGTCACTCGTGTGGGTGGTCATCATACACACAAAGGCCAGGAATGAAGA
TTGCACTACCAACACAGATGAGACCAACTTGCAGCAGGATATTCTAGTTATTGTGTCATCTCAGGGAAACGTT
AGCTGACAGGCAGGATGGGTACGTGCTTCAGAAAGTGGAAAGCCACACCAGTTGTCACATCTTCAGGTGCTGG
ATTTTCTTACACACATGACAGTAGTGGGACCTGCCATTGACAATAGCAGTGAAGCTGATGGAAGCTGCC
CACAGATCTGTCCTTGTCCGTTGGATCCACAGGCCATATGTTGAAAGGAAATGTGTATGGCTCAGA
TCCTTTGAAACATATCATACAGGTGCACTGCAGTCCTGACCCAAAGAACAGTTTAATGGACCACTATGAGCCAGTTA
CATAAAGAAAAGGAGTGTACCCATGTTCTCATCTTCAGAAAGAACCTGCAAGGGAGCTTCAGTAATATATC
GTGGCCTTCACATGTGAGGAAGCTACTAACACTAGTTCTCACAATGAAGGACCTGGAAATGAAAATCTGTG
TCTAAACAAGTCCTCTTAGTTAGTTAGTGCACCATCCAGAGGCCAGCGTCGGTTGCCAGTAATTCTCATGGG
TACCTTGGAAAAGCTCTCAGGAGACCTCACCTAGATGCTTATTCAAGCTTGGACAGCCATCAGATTGTCAGCC
AAGAGCCTTTATTGAAAGCTCATCTTCCCCAGACTGGACTCTGGGTAGAGGAAGATGGAAAGAAAGGAC
AGATTTCAAGGAAAGAAATCACATTGTCACCTTAAACAGACTTAAAGGAAACTACAGGACTCCAAATTTCAGTC
TTATGACTTGGACACATAGACTGAATGAGACCAAGGAAAGCTTAACACATACTACCTCAAGTGAACTTTATT
AAAGAGAGAAATCTTATGTTAAATGGAGTTATGAATTAAAGGATAAAATGCTTATTATACAGAT
GAACCAAATTACAAAAAGTATGAAAATTITATACTGGGAATGATGCTCATATAAGAATACCTTTAAACTA
TTTTTAACTTTGTTTATGCAAAAAGTATCTACGTAATTAAATGATATAAAATCATGATTATTTATGTATTT
TTATAATGCCAGATTCTTATGAAAATGAGTTACTAAAGCATTTAAATAACCTGCCCTGTACCAATT
TTAAATAGAAGTTACTTCATTATATTGCACTTAAATTTGAA

FIGURE 102

MVDVLLLFSLCLLFHISRPDLSHNRLSFIKASSMSHLQSLREVKLNNELETIPNLGPVSAN
ITLLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEP
GYFDNLANTLLVLKLNRRNRIASAIPPKMFKLPQLQHLELRNKKIKNVDGLTFQGLGALKSLKM
QRNGVTKLMMDGAFWGLSNMEILQLDHNNLTEITKGWLYGMLQELHLSQNAINRISPDAWE
FCQKLSELDLTFNHLSRLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRLSSLKTLIDLKNNE
ISWTIEDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLOQNAFSQ
MKKLQQLHLNTSSLLCDCQLKWLPOWVAENNFSQSFVNASCAPQLLKGRSIFAVSPDFVCD
DFPKPQITVQPETQSAIKGSNLNFICSAASSDSPMTFAWKKDNEELLHDAEMENYAHLRAQG
GEVMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVNMLPSFTKTPMDLTIRAGA
MARLECAAVGHPPAQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQN
SAGSISANATLTVLETPSFLRPLLDRTVKGETAVLQCIAGGSPPKLNWTKDDSPVVTER
HFFAAGNQLLIIVDSDVSDAGKYTCEMSNTLGTERGNVRLSVIPTPTCDSPQM TAPS LDDDG
WATVGVIIIAVVCVVGTSLVWVVIYHTRRRNEDCSITNTDETNL PADIPS YLSSQGT LAD
RQDGYVSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLFLCPFLGSTGP
MYLKGNVYGSDPFETYHTGCSPDPRTVLMHYEPSYIKKKECYPCHPSEESCRFSNISW
PSHVRKLLNTSYSHNEGPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDA
YSSFGQPSDCQPRAFYLKAHSSPDLD SGSEEDGKERTDFQEENHICTFKQTLENY RTPNFQS
YDLDT

Signal sequence:

amino acids 1-19

Transmembrane domain:

amino acids 746-765

N-glycosylation site.

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 103

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTTGGTGGTGGCTGGCTGGGCCTTGCAAAAATG
AAGGATGCAGGACGCAGCTTCCTGGAACGCAACGCAATGGATAACTGATTGTCAAGAGAGAAGGAAGAAC
GAAGCTTTCTGTGAGCCCTGGATCTAACACAATGTGTATATGTGCACACAGGGAGCATTCAAGAAATGAAA
TAAACCAGAGTTAGACCCGGGGGTGGTGTGTTCTGACATAATAATCTAAAGCAGCTGTCCTCC
CCACCCCCAAAAAAAGGATGATTGGAAATGAAGAACCGAGGATTCAAAGAAAAAGTATGTTCATTTCTC
TATAAAGGAGAAAGTGAGCCAAGGAGATATTTGGAATGAAAAGTTGGGGCTTTTAGTAAAGTAAGAAACT
GGTGTGGTGGTGTTCCTTCTTTGAAATTCCCACAAGAGGAGAGGAAATTAAATAATACATCTGCAAAGAAA
TTTCAGAGAAGAAAAGTTGACCGCGGAGATTGAGGCATTGAGGATTGGGGAGAGAAACCAGCACAGTTGGA
TTTGTGCCTATGTTGACTAAAATTGACGGATAATTGCACTGGATTTCATCAACCTCTTTTTTAAAT
TTTATTCCCTTGGTATCAAGATCATGCGTTCTCTGTTCTAACACCTGGATTTCATCTGGATGTTGCT
GTGATCAGTCTGAAATACAACGTGTTGAAATTCCAGAACAGGACAAACACAGATAAAATTATGAATGTTGAACAGAT
GACCTACATCCACAGCAGATAATGATAGGTCTAGGTTAACAGGGCCCTATTGACCCCTGCTGTGGTGT
GCTGGCTCTCAACTCTTGTGGCTGGCTGGTGCAGACCTGCCCTCTGTGTGTCCTGCAGCAA
CCAGTCAGCAAGGTGATTGTGTCGGAAAAACCTGCGTAGGTTCCGGATGGCATCTCCACCAACACAGGCT
GCTGAACCTCCATGAGAACCAAATCCAGATCATCAAAGTGAACAGCCTCAAGCAGGACTTGGAAATCCT
ACAGTTGAGTAGGAACCATATCAGAACATTGAAATTGGGCTTCATGGTCTGGCAACCTCAACACTCTGGA
ACTCTTGACAATCGTCTTACTACCATCCGAATTGGAGCTTTGTATACTTGCTAAACTGAAGGAGCTGGTT
GCCAACAAACCCATTGAAAGCATCCCTCTTACAGAACATTGGGAGCTGGCAGCTAGAACATTGAG
GGAATTGAAAAGACTTTCATACATCTCAGAACGGCTTGTGAAAGGTCTGTCCAACCTGAGGTATTGAAACCTTG
CATGTGCAACCTCGGGAAATCCCTAACCTCACACCGCTCATAAAAGTGAACAGCCTGGATCTGGGAAATCA
TTTATCTGCCATCAGGCCCTGGCTCTTCCAGGGTTGATGACACCTTCAAAACTGTGGATGATACAGTCCAGAT
TCAAGTGATTGAAACGAATGCCTTGACAACCTTCACTGACTAGTGGAGATCAACCTGGCACACAATAATCTAAC
ATTACTGCCTCATGACCTCTTCACTCCCTGCATCATCTAGAGCGGATACATTACATCACACACCTTGGAAACTG
TAACGTGACATACTGTGGCTCAGCTGGTGGATAAAAGACATGGCCCCCTCGAACACAGCTTGTGCCCCGTG
TAACACTCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTGACCAGAACATTACTCACATGCTATGCTCCCGT
GATTGTGGAGCCCCCTGCAGACCTCAATGTCAGTGAAGGCATGGCAGCTGAGCTGAAATGTGGGCTCACATC
CCTGACATCTGTATCTGGATTACTCCAAATGGAACAGTCATGACACATGGGCGTACAAAGTGCAGGATAGCTGT
GCTCAGTGTGGTACGTTAAATTCAAAATGTAACGTGCAAGATAACAGGCATGTACACATGTATGGTGGTAA
TTCCGGTGGGAAATACTACTGCTTCAGCCACCTGAATGTTACTGCAGCAACCACACTCCTTCTTACTTTTCA
AACCGTCACAGTAGAGACTATGAAACCGTCTCAGGATGAGGCACGGACCACAGATAACAATGTGGGCTCCACTCC
AGTGGTCAGTGGAGACCACCAATGTGACCACCTCTCACACCACAGGCACAAGGTGACAGAGAAAACCTT
CACCACCCAGTGACTGATAAAACAGTGGATCCAGGAATTGATGAGGTCTGAAGACTACCAAAATCATCAT
TGGGTGTTTGTGGCATCACACTCATGGCTGCAGTGTGCTGGTCAATTCTACAAGATGAGGAAGCAGCACCA
TCGGCAAAACCATCACGCCAACAGGACTGTTGAAATTATAATGTGGATGATGAGGATACGGGAGACACACC
CATGGAAAAGCCACCTGCCATGCCGTATCGAGCATGAGCACCTAAACTATAACTCATACAATCTCCCTT
CAACACACAAACAGTTAACACAATAAAATTCAATACACAGTTCACTGCAACCGTTATTGATCCGAATGAA
CTCTAAAGACAATGTACAAGAGACTCAAATCTAAACATTTACAGAGTTACAAAAAAACAAACAAATCAAAAAAA
GACAGTTTATTAAGACACAAATGACTGGCTAAATCTACTGTTCAAAAAAGTGTCTTACAAAAAAACAA
AAAAGAAAAGAAATTATTTATTAAGCAGACAAAAA

FIGURE 104

MLNKMTLHPQQIMIGPRFNRALFDPLLVLALLQLLVVAGLVRAQTCPSVCSCSNQFSKVIC
VRKNLREVPDGISTNTRLLNLHENQIQIICKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA
NLNTLELFNDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS
YISEGAFEGLSNLRYLNLCNLREIPNLTPLIKLDELDLSGNHLSAIRPGSFQGLMHLQKL
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLPHDLFTPPLHHLERIHLHHNPWCNCIDIL
WLSWWIKDMASTSNTACCACRNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNTEGMAAE
LKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQDTGMYTCMVSNSVGN
TTASATLNVTAAATTTPFSYFSTVTVETMEPSQDEARTTDNNVGPTVVDWETTNVTTSLTPQ
STRSTEKTFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQN
HHAPTRTVEIINVDEITGDTPMESHLPMPAIEHEHLNHYN SYKSPFNHTTVNTINSIHSS
VHEPLLIRMNNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,
442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
391-397, 422-428, 433-439, 531-537

FIGURE 105

AGCCGACGCTGCTCAAGCTGCAACTCTGGCAGTTGGCAGTCTTCCGTTCCCTGCTGTTGGGGCA
TGAAAGGGCTCGCCGGGAGTAAGGAATTGACCGGGCAGCGCAGGGAGCGCGCACCGCACCG
GAGGGCGGGCGTGCACCCCTCGCTGGAAGTTGTGCCGGGCCCCGAGCGCGCCGGCTGGAGCTCGGGTAGA
GACCTAGGCCGCTGGACC~~CG~~GTAGCGCGCAGCCTCCGTGCGCGCCGGGTTGGGCTGCTGTC
GCGGTGCTGGGCGCTGGCGGTCCGACAGCGGGCTCGCGGGAACTCGGGCAGCCCTGTTGGTAGCCGCC
GAGCGCCCATGCCCAACTACCTGCCGCTGCCCTGGGACTCTGAGTCAGTCAGGCTAGCGCTCTT
CCCGAGCCACTCCCCTGGCTGCTCGGCTGGACTTAAGTCACAACAGATTATCTTCAAGGCAAGTTCC
ATGAGCCACCTCAAGCCTCGAGAAGTGAACAACTGAATTGGAGACCATTCCAATCTGGGACCA
GTCTCGGCAAATATTACACCTCTCTGGCTGGAACAGGATTGTTGAATACTCCCTGAACATCTGAAAGAG
TTTCAGTCCCTGAAACTTTGACCTTAGCAGCAACAAATTTAGCTCAGGCTCCAAACTGCATTCCAGGCCACAG
CTCAAATATCTGTATCTCAACAGCAACCCAGTCACATCAATGAAACCTGGTATTGACAATTGGCCAACACA
CTCTCTTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCCACCCAAGATGTTAAACTGCCAACATGCAA
CATCTCGAAATTGAAACCGAAACAGATTAAAGTAGATGGACTGACATTCCAAGGCCCTGGTCTGCTGAAAGTCT
CTGAAAATGCAAAGAAATGGAGTAACGAAACTATGGATGGACTTGGGGCTGAGAACATGGAATTG
CAGCTGGACCATAACAAACCTAACAGAGATTACCAAAGGCTGGCTTACGGCTGCTGAGCTGAGGACTTCA
CTCAGCCAAATGCCATCAACAGGATCAGCCCTGATGGCTGGAGTCTGCCAGAACGCTCAGTGAGCTGGACCA
ACTTCAATCACTTACAGGTTAGATGATTCAAGCTCCTGGCTTAAGCTTACTAAATACACTGCACATTGG
AAACAACAGAGTCAGCTACATTGCTGATTGCTTCCGGGGCTTCCAGTTAAAGACTTTGGATCTGAAAGAAC
AATGAAATTCTCGGACTATTGAAGACATGAATGGTGTTCTGGGCTGACAAACTGAGGCGACTGATAACTC
CAAGGAAATCGGATCCGTTCTATTACTAAAAAGCCTTCACTGGTTGGATGCATTGGAGCATCTAGACCTGAGT
GACAACCCAATCATGTCTTACAAGGCAATGCAATTGACAAACTGCAACAATTGCAATTAAATACA
TCAAGCCTTGTGCGATTGCCAGCTAAATGGCTCCACAGTGGTGGGGAAAACAACCTTCAGAGCTTGT
AATGCCAGTTGTGCCCATCCTCAGCTGCTAAAGGAAGAAGCATTGGCTGTTAGCCAGATGGCTTGTG
GATGATTTCCTCAAACCCAGTCAGGGTCAAGGCAAAACAGTCGGCAATAAAAGGTTCAATTGAGTT
ATCTGCTCAGCTGCCAGCAGCAGTGATTCCCAATGACTTTGCTTGGAAAAAGACAATGAACTACTGCATGAT
GCTGAAATGAAAATTATGACACCTCCGGGCCAAGGTGGCAGGTGATGGAGTATACCACATCCTCGGCTG
CGCAGGGTGAATTGCCAGTGAGGGAAATATCAGTGTGTCATCTCAAATCAGTTGGTCTCATCCTACTCTGTC
AAAGCCAAGCTTACAGTAAATATGCTTCCCTCATTCAACAGACCCCCATGGATCTCACCATCCGAGCTGGGGCC
ATGGCACCTGGAGTGTGCTGTGGGCCACCCAGCCCCCAGATAGCTGGCAGAAGGATGGGGCAGAC
TTCCAGCTGCCAGGGAGAGACGCTAGTGTGATGCCAGGATGACGTTCTTATGTTGAGTGTGAAAGATA
GAGGACATTGGGTATACAGCTGCACAGCTCAGAACAGTGCAGGAAGTATTGCAACATGCAACTCTGACTGTC
CTAGAACACCATCATTTGCCACTGTTGGACGAATGTAACCAAGGGAGAAACAGCGCTTACAGTGC
ATTGCTGGAGGAAGCCCTCCCCCTAAACTGAACTGGACCAAAGATGATAGCCCATTGGTGGTAACCGAGAGGCAC
TTTTTGAGCAGGCAATCAGCTCTGATTATTGAGACTCAGATGTCAGTGATGGAAATACACATGTGAG
ATGTCTAACACCCCTGGCACTGAGAGAGGAAACGTGCGCCTCAGTGTGATCCCCACTTCAACCTGCGACTCCCC
CAGATGACAGCCCCCATCGTAGACGATGCGATGGGCCACTGTGGGTGCTGATCATAGCGTGGTTGCTG
GTGGTGGGACGTCACTCGTGTGGGTGGTATCATATACCACACAAGGGAGGAATGAAAGATTGCGAGCATTACC
AACACAGATGAGACCAACTTGCAGCAGATATTCTAGTTATTGTCATCTCAGGGACGTTAGCTGACAGGCAG
GATGGGTACGTGCTTCAGAAAGTGGAGCCACCCAGTTGTCACATCTCAGGTGCTGGATTGTTCTACCA
AACATGACAGTAGTGGACCTGCCATATTGACAATAGCAGTGAAGCTGATGTGGAAAGCTGCCACAGATCTGTC
CTTGTCCGTTTTGGATCCACAGGCCATTGTTGAAGGGAAATGTTGCTCAGATCTTGTAAACA
TATCATACAGGTTGCACTGCCAGAACAGTTAAATGGACCAACTGAGCCCAGTTACATAAAGAAAAG
GAGTGCTACCCATGTTCTCATCTTCAGAAGAATCTGCGAACGGAGCTCAGTAATATATGTCAGGCTTACAT
GTGAGGAAGCTACTTAAACACTAGTTACTCTCACAATGAAGGACTGGAATGAAAATCTGTCATAACAGTCC
TCTTGTGATTGAGTGTGAAATCCAGGCCAGCGTCGGTGTGCTCGAGTAATTCTTATGTCAGGTTACCTTGGAAAA
GCTCTCAGGAGACCTCACCTAGATGCTTACAGTGTGAGGCCAGTGGACAGGAACTGAGGAGGAGGAGGAG
TTGAAAGCTATTCTTCCCGACTGGCTAGGGTCAAGGAGATGGAAAGAAGGAGCAGATTTCAGGAA
GAAAATCACATTGAGTCTTAAACAGACTTAAAGGAAAGCTTAAACATACACTACCTCAAGTGAACCTT
ACATAGACTGAATGAGACCAAGGAAAGCTTAAACATACACTACCTCAAGTGAACCTTATTAAAGAGAGGAG
CTTATGTTTTAAATGGAGTTATGAAATTAAAGGATAAAATGCTTATTATGTCAGGTTACCTTGGAAAA
AAAAAGTTATGAAAATTTTATGAGGAAATGATGCTCATATAAGAATACCTTTAAACTATTTTAACTT
TTTATGCAAAAAGTATCTACGTTAAATTAAATGATAATTATGATTATTGTTATGTCAGGTTACCTTGGAC
TTCTTGTGAAATGGAAATGAGTTACTAAAGCATTAAATAACCTGCTTGTACCATTTTAAATAGAAGTT
ACTTCATTATATTGCACTTAAATGAGTCAATTGAAAAAAAAAAAAAAAAAAAAAA

FIGURE 106

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGGRGELGQPSGVAAPERCPPTCRLGDLLDCSR
KRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSANIT
LLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFFPALQLKYLYLNSNRVTSMEPGY
FDNLANTLLVLLKLNRRNISAIPPKMFKLPOLOHLELRNKKNVDGLTFQGLGALKSLKMQR
NGVTKLMGAFWGGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAINRISPAWEFC
QKLSELDLTFNHLSRLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRLSSLKTLSDLKNNEIS
WTIEDMNGAFSGLDKLRRRLILQGNRIRISITKAFTGLDALEHLDLSDNAIMSLQGNAFSQMK
KLQLHLNTSSLLCDCQLKWLPOWVAENNQSFVNASCAPQOLLKGRSIFAVSPDGFVCDDF
PKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKDNELLHDAEMENYAHLRAQGGE
VMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTNVNMLPSFTKTPMDLTIRAGAMA
RLECAAVGHPPAQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQNSA
GSISANATLTVLETPSFLRPLLDRVTKGTAVALQCIAGGSPPPQLNWTKDPSPLVVTERHF
FAAGNQLLIIVDSDVSAGKYCEMSNTLGTERGNVRLSVIPTPTCDSPQMGTAPSLLDDGWA
TVGVVIIAVVCCVVGTSLVWVVIYHTRRRNEDCSITNTDETNLPADIPSYLSSQGTIADRQ
DGYVSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEATDLFLCPFLGSTGPMY
LKGNVYGSDFETYHTGCSPDPRTVLMHYEPSYIKKKECYPCHSEESCERSFSNISWPS
HVRKLLNTSYSHNEPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDAYS
SFGQPSDCQPRAFYLKAHSSPDLDSGSEEDKERTDFQEENHICTFKQTLNEYRTPNFQSYDLDT

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 808-828

N-glycosylation site.

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519, 688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

Glycosaminoglycan attachment site.

amino acids 886-890

Casein kinase II phosphorylation site.

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378, 383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735, 799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022, 1073-1077, 1079-1083, 1081-1085

Tyrosine kinase phosphorylation site.

amino acids 667-675

N-myristoylation site.

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433, 513-519, 588-594, 672-678, 683-687, 774-780, 933-939

Leucine zipper pattern.

amino acids 58-80, 65-87

FIGURE 107

CAAAACTTGCCTCGCGGAGAGCGCCCAGTTGACTTGAATGGAAGGAGCCCGAGCCCGCGAGCGCAGCTGAGAC
TGGGGAGCGCGTTCGGCCGTGCCCCGCGCTCGGCCGGGGCGCAGCAGGGAGGGAAAGCTGTGGTCTGCC
CTGCTCCACGAGGCCTGAGCTGGTGTGAACCGGGAGAGCCCCCTGGTGGTCCCTATCCCTCTTATATA
GAAACCTTCCACACTGGAAAGGAGCAGCGCGAGGAGGAGGCTATGGTGAAGCAAGGAGGCCGCTGATCTGCAG
GCGCACAGCATCCGAGTTACAGATTACAGATACCAAATGGAAGGCGAGGAGGAGGAGAACAGCCTGCCGTGGT
TCCATCAGCCCTGGCGCCAGCGCAGTCAGCTGCCACCCCTGCAGGCACCCTGGCCAGAGCCGGGTGCTGC
TGCTCCTGCTGCTGCCACAGCTGCACCTGGACCTGTGCTTGCCTGAGGGCCAGGATTGGCCGAA
GTGGGGCCACAGCCTGAGCCCCAGAGAACGAATTGGCCAGGAGGAGGCCGCTGGTACTGAGCCCTGAGG
AGCCCCGGCTGGCCAGCCGCGTCACTGCCCGAGACTGTGCTGCTTCCAGGAGGCCGCTGGACTGTG
GCGTATTGACCTGCGTGAAGTCCCGGGGACCTGCCTGAGCACACCAACCTATCTGAGAACACAACCAGC
TGGAAAAGATCTACCTGAGGAGCTCTCCGGCTGCACCGGGCTGGAGACACTGCAACACTGCAA
AAACACAACCGCCTGA
CTTCCCAGGGCTCCAGAGAAGGCTTGAGCATCTGACCAACCTCAATTACCTGACTTGCCAATAACAAGC
TGACCTTGGCACCCGCTTCTGCAAACGCCGTGATCAGTGTGACTTGCTGCAACTATCTACCAAGATCT
ATGGGCTCACCTTGGCCAGAACGCAAACCTGAGGTCTGTGACCTGACAACAAGCTGGCAGACGCCGGC
TGCCGGACAACATGTTCAACGGCTCCAGCAACGTGAGGTCTCATCTGTCAGCAACTTCTGCGCCACGTG
CCAAGCACCTGCCCTGCCCTGTAAGACTGCAACCTCAAGAACACAAGCTGGAGAAGATCCCCCGGGGCCT
TCAGCGAGCTGAGCAGCTGCCAGCTATACTGAGAACAACTACCTGACTGACGAGGGCTGGACAACGAGA
CCTTCTGGAAGCTCTCAGCCGGAGTACCTGGATCTGTCAGCAACAACTGTCTGGTCCAGCTGGGCTGC
CGCGCAGCCTGGTCTGCACTTGAGAAGAACGCCATCCGGAGCGTGGACGCCAATGTGCTGACCCCCATCC
GCAGCCTGGAGTACCTGCTGTCAGCAACCGAGCTGCCAGGAGCAGGGCATCCACCCACTGGCTTCCAGGGC
TCAAGCGTTGACACGGTGCACCTGTAACAAACAGCGCTGGAGCGCTGCCAGTGGCTGCCGCGTGC
GCACCCATGATCCTGACAACCGAGTACAGGCAATTGGCGCGAAGACTTGGCACCACCTACTTCTGGAGG
AGCTCAACCTCAGCTACACCGCATCACCAGGCCACAGGTGCAACGCCCTTCCGCAAGCTGCGCTGCTGC
GCTCGCTGGACCTGTCGGCAACCGGCTGCACACGCTGCCACCTGGCTGCGCTCGAAATGTCCATGTGCTGAAGG
TCAAGCGCAATGAGCTGGCTGCTGGCAAGGGGGCTGGCGTGGCGGGCATGGCTCAGCTGCGTGAAGTACCTCA
CCAGCAACCGACTGCGCACGGAGCCCTGGGCCCCGGTGGCTGGACCTCGCCATCTGAGCTGCTGGACA
TCGCCGGAAATCAGCTCACAGAGATCCCCGAGGGCTCCCGAGTCACTTGAGTACCTGACCTGAGAACAAACA
AGATTAGTGCGGTGCCGCCAATGCTTCGACTCCACGCCAACCTCAAGGGATCTTCTCAGGTTAACAAAGC
TGGCTGTGGGCTCCGTGGTGGACAGTGCCTTCCGGAGGCTGAAGCACCTGCAAGGTCTGGACATTGAAGGCAACT
TAGAGTTGGTGAACATTCCAAGGACCGTGGCCCTTGGGAAGGAAAAGGAGGAGGAGGAAGAGGAGGAGG
AGGAAGAGGAAACAAGATAGTGACAAGGTGATGAGATGTGACCTAGGATGATGGACCGCCGACTTTCTGC
AGCACACGCCGTGCTGCTGAGCCCCCACTCTGCCGTGTCACACAGACACACCCAGCTGCACACATGAGGCA
TCCCACATGACACGGGCTGACACAGTCTCATATCCCCACCCCTCCACGGCGTGTCCCACGGCCAGACACATGC
ACACACATCACACCCCTCAAACACCCAGCTCACCCACACAACTACCCCAAACACCAAGTCTGTCACAC
CCCCACTACCGCTGCCACGCCCTCTGAATCATGAGGGAGGGCTGCCCTGGCACACACAGGCC
TTCCCTCCCCCTGCTGACATGTGATGCGTATGCAACACACACACACATGACAAGTCATGTGCGAA
CAGCCCTCAAAGCCTATGCCACAGACAGCTTGCCTGCCAGGAATCAGCCATAGCAGCTGCCGTGCG
GTCCATCTGCCGTCCGTTCCCTGGAGAAGACACAAGGGTATCCATGCTCTGCTGCCAGGGCTGCCACCC
GGAACCTCACAAAAGCTGGCTTTATTCCCTTCCATCCTATGGGAGGGACTCAGGACTGCTGGCC
TGGCCCACCCCTGCTCCAGGTGCTGGCAGTCACTCTGCTAAGAGTCCCTCCCTGCCACGCCCTGGCAGGACA
CAGGCACTTTCCAATGGGCAAGGCCAGTGGAGGAGGAGGAGGCCCTGGGTGCTGGGGCCTGGGG
CAGGAGTGAAGCAGAGGTGATGGGCTGGCTGAGCCAGGGAGGAAGGACCCAGCTGCACCTAGGAGAACCTT
GTTCTCAGGCCGTGGGGAGGTTCCGGGTGCCCTTATTCTTATTCTTCTAAGGAAAAAATGATAAAAAT
CTCAAAGCTGATTTCTTGTATAGAAAAACTAATATAAAAGCATTACCCATCCCTGCAAAAAAA

FIGURE 108

MEGEEAEQPAWFHQWPWRPGASDSAPPAGTMAQSRVLLLLLPPQLHLGPVLAVRAPGFGRS
GGHSLSPPEENFAEEEPLVLSPEEPGPAAVSCPRDCACSQEGVVDCGGIDLREFPGDLP
EHTNHLSLQNNQLEKIYPEELSRLHRLETNLQNNRRLTSRGLPEKAFFEHTNLNYLYLANNK
LT LAPRFLPNALISVDFAANYLT KIYGLTFGQKP NLRSVY LHNNKLADAGLPDNMFNGSSNV
EV LILSSNFLRHPKHLPPALYKLHLKNNKLEKIPPGAFSELSSLRELYLQNNYLTDEGLDN
ET FWKLSSLEYLDLSSNNLSRVPA GLP RSLVLLHLEKNAIRSDANVLPIRSLEYLLLHSN
QLREQGIHPLAFQGLKRLHTVHLYNNALERVPSGLP RRVRTLMILHNQITGIGREDFATTYF
LEELNLSYNRITSPOVHRDAFRKLRLRSLDLSGNRLHTLPPGLPRNVHVLKVKRNEALAALA
RGALAGMAQLRELYLTSNRRLRSRALGPRAWVDLAHLQ LLDIAGNQLTEIPEGLPESLEYLYL
QNNKISAVPANA FDSTPNLK GIFLRFNKLAVGSVVDSA FRRLKHLQVLDIEGNLEFGDISKD
RGRLGKEKEEEEEEEEEEETR

Signal sequence:

amino acids 1-48

N-glycosylation site.

amino acids 243-247, 310-314, 328-332, 439-443

Casein kinase II phosphorylation site.

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

N-myristoylation site.

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,
477-483, 498-502, 539-545, 548-554

Leucine zipper pattern.

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,
535-557

FIGURE 109

GGGAGGGGGCTCCGGCGCCGCGCAGCAGACCTGCTCCGGCGCGCCCTGCCGCTGTCCTCCGGAGCGGCAG
CACTAGCCGGCGGGAGGGCTGGGGTTCTCGAGACTCTCAGAGGGGCGCTCCCATCGGCCACCACCC
CAACCTGTTCTCGCGGCCACTCGCTCGGCCAGGACCCGCTGCCAACATGGATTCTCTGGCGTGT
GCTGGTATCCTCGCTCACCTGCAAGGGCGCGAGTTCGACGGGAGGGTGGGCCAGGCAAATAGTGTATCGAT
TGGCCTATGTCGTTATGGTGGAGGATTGACTGCTGCTGGGGCTGGGCTGCCAGTCTGGGACAGTGTAGCC
TGTGTGCCAACACCAGATGCAAACATGGTAATGTATCGGGCAAACAAGTGAAGTGTATCTGGTTATGCTGG
AAAAACCTGTAATCAAGATCTAAATGAGTGTGGCTGAAGCCCCGGCCCTGAAGCACAGGTGATGAACACTTA
CGGCAGCTACAAGTGTACTGCTCAACGGATATGCTATGCCGATGTTCTGCTCAAGTGCCTGACCTG
CTCCATGGCAAACGTCACTGATGGCTGTGATGTTAAAGGACAAATACGGTGCCTAGGCCATCCCCTGGCCT
GCACCTGGCTCTGATGGAGGACCTGTTAGATGTTGATGAATGTGCTACAGGAAGAGCCTCTGCCCTAGATT
TAGGCAATGTCACACTTTGGGAGCTACATCTGCAAGTGTCTAAAGGCTTCGATCTCATGTATATTGGAGG
CAAATATCAATGTCATGACATAGACGAATGCTCACTGGTCACTGTCAGTGCAGCAGCTTGCTCGATGTTAA
CGTAGTGGCTCTACAAGTGCACATGAAAGGATAACCAAGGGTGTGACTGACTGTTGTTGATATCCC
AGTTATGATTGAAACCTCAGGTCAAATTCTAGTACCAAAGGGAAATGGTACCTTTAAAGGGTACACAGGAAA
TAATAATTGGATTCTGATGTTGAAAGTACTTGGTGGCTCCGAAAGACACCATATCTCTCTATCATTACCAA
CAGGCTACTTCTAAGGCAACAAAGACCTACACCAAAGGCAACACCAAATTCTACTCCACCACCA
CTGCCAACAGAGCTCAGAACACCTCTACACCTACACCCCCAGAAAGGCCAACACCGGACTGACA
ACCAGCTGCCAGTACACCTCCAGGGATTACAGTTGACAACAGGGTACAGACAGACCCCTCAGAAACCC
AGAGTGTTCAGTGTCTGGTACACAGTTGAAATTGACCATGGACTTGTGGATGGATCAGGGAGAAAGACAA
TGACTTGCACTGGGACCAATCAGGGACCCAGCAGGTGGACAATATCTGACAGTGTGGCAGGCC
GGGAAAGCTGCACGCTTGGTGTACCTCTGGCCCTATGCATTCAAGGGACCTGTGCTGTCAATT
CAAGGTGACGGGGCTGCACTTGGCACACTCCAGGTGTTGTGAGAAAACAGGTGCCACGGAGCAGCC
GGGAAGAAAATGGTGGCCATGGCTGGAGGAAACACAGATCACCTTGGAGGGGCTGACATCAAGAGCGA
AAAGATGATTAAAGGGTTGGAAAAAAAAGATCTATGATGGAAAATTAAAGGA
AGATGACTGAGGGGCAACCAATTGATGGTTTCAAGTATATGAAGGGTTGG
TTCTCCATATGCACTAAGAATAGAACAGAGGAAACTGGCTTAGACTAGAGTATAAGGGAG
GGCCATTGTTAGAATACTTCATAAAAAAAGAAGTGTGAAATCTCAGTATCTCTCTTCTAA
AAAAAATTGTCATTTAAGATGGTTAAAGATGTTCTACCCAGGAAAGTA
AGATGTTTGTACTAGTAGTATGCACTGAAATCTTAAAGACTAAATAATT
CATTTCCCTCTGACCTCTTAATGGAGAGGGATTGAAAGGGGAAGAG
AGATATTGTTAGTATCTCAGTAATGCTCTAGTGTGGCGGTGTTCA
TTTCATTGTTCAATGGATGATGTTCAAGGAGATCTTCAAGGA
ATTTTCATGGGTGCAATTCTCTGCTTCTGTCAGAAGTATTCT
ACACCGGCAGACCTTCTCTACCTCATCAGTATGATTCA
AGAACAGTAATATTGAAACAATAGGTACAATAGAAGGGTCT
AGGGGGAAAATAAATCATTAAAGCCTTGA
TGATACATTGCACTAAACTGATGGAAGAAGTTATCCA
CTAAAATAAAAAATGTTAGTGGTTTCAAATGCC
TGAAATAAAACAATTGTA
TGAAATAAAACAGTGTAGTAAT

FIGURE 110

MDFLLALVLVSSLYLQAAAEDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVCP
RCKHGE CIGPNKCKCHPGYAGKTCNQDLNECGLKPRPC KHRCMNTYGSYKCYCLNGYMLMPD
GSCSSALTCSMANCQYGCDVVKGQIRCQCPSPGLHLAPDRTCDVDECATGRASCPRFRQC
VNTFGSYICKCHKGFDL MYIGGKYQCHDIDECSLGQYQCSSFARCYNVRGSYKCKCKEGYQG
DGLTCVYIPKVMIEPSGPIHVPKGNGTILKGDTGNNNWI PDVGSTWWPPKTPYIPPIITNRP
TSKPTTRPTPKPTPIPTPPPPPPLPTELRTPPLPPTPERPTTGLTTIAPA AASTPPGGITVDN
RVQTDPQKPRGDVF SVLVHSCNF DHLGCGWIREKDNDLHW EPIRD PAGGQYLTVA AKAPGG
KAARLVLPLGRLMHSGDLCLSFRHKVTGLHS GTLQVFVRKHGA ALWGRNGGHGW RQTQI
TLRGADI KSESQR

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 273-277

Casein kinase II phosphorylation site.

amino acids 166-170, 345-349

Tyrosine kinase phosphorylation site.

amino acids 199-206

N-myristoylation site.

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,
421-427, 433-439, 462-468, 476-482

Aspartic acid and asparagine hydroxylation site.

amino acids 104-116, 186-198, 231-243

Cell attachment sequence.

amino acids 382-385

EGF-like domain cysteine pattern signature.

amino acids 75-87

FIGURE 111

CTTCTTTGAAAAGGATTATCACCTGATCAGGTTCTCTGCATTCGCCCTTAGATTGTGA
AATGGCTCAAGGTCTCACAACTTCCCTTGCAACAGGTGCTGCTCGGGGCTGA
AGGTGACAGTGCATCACACACTGTCCATGGCGTCAGAGGTCAAGGCCCTACCTACCCGTC
CACTATGGCTCCACACTCCAGCATCAGACATCCAGATCATGGTATTGAGAGACCCCA
ACAATGCCAAATACCTACTGGGCTCTGTGAATAAGTCTGTGGTCCTGACTTGAATACC
AACACAAGTTCACCATGATGCCACCCAAATGCATCTGCTTATCAACCCACTGCAGTCCCT
GATGAAGGCAATTACATCGTGAAGGTCAACATTAGGGAAATGGAACTCTATGCCAGTCA
GAAGATAACAAGTCACGGTTGATGATCCTGTACAAAGCCAGTGGTCAGATTCACTCCTCC
CTGGGCTGTGGAGTATGTGGGAACATGACCTGACATGCCATGTGGAAGGGGGACTCGG
CTAGCTTACCAATGGCTAAAAATGGGAGACCTGTCCACACCAGCTCCACCTACTCCTTT
TCCCCAAAACAATACCCTCATATTGCTCCAGTAACCAAGGAAGACATTGGAATTACAGCT
GCCTGGTGAGGAACCTGTCAGTGAAATGAAAGTGAATATCATTATGCCATCATATTAT
GGACCTTATGGACTTCAAGTGAATTCTGATAAAGGGCTAAAAGTAGGGGAAGTGTACTGT
TGACCTTGGAGAGGCCATCCTATTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACT
CCTGGATTAGGAGGACTGACAATACTACATATCATTAAGCATGGCCTCGCTTAGAAGTT
GCATCTGAGAAAGTAGCCCAGAAGACAATGGACTATGTGTGCTGCTTACAACAACATAAC
CGGCAGGCAAGATGAAACTCATTCACAGTTATCATCACTCCGTAGGACTGGAGAAGCTTG
CACAGAAAGGAAATCATTGTCACCTTAGCAAGTATAACTGGAATATCACTATTTGATT
ATATCCATGTGTCCTCTTCTATGGAAAAAATATCAACCCATAAAAGTTAAAAACAGAA
ACTAGAACGCCAGAAACAGAACATAGGAAAGCTCAAACATTTCAGGCCATGAAGATG
CTCTGGATGACTTCGGAATATGAATTGTTCTCAGATGTTCTGGTGTGTTCCAGG
ATTCCAAGCAGGTCTGTTCCAGCCTCTGATTGTATCGGGCAAGATTGACAGTACAGT
GTATGAAGTTATTCAAGCACATCCCTGCCAGCAGCAAGACCATCCAGAGT**TGA**ACTTCTATGG
GCTAACAGTACATTGAGTGAAGAAACATTGAAGAAACATTAAAGGAAAACAGTGGAAAAGT
ATATTAATCTGGAATCAAGTGAAGAAACCAGGACCAACACCTCTTACTCATTATTCTTACA
TGCAGAACAGGATTATGCAAATTGAACTGCAGGTTTCAGCATATAACAAATGTCTT
GTGCAACAGAAAACATGTTGGGAAATATTCTCAGTGGAGAGTCGTTCTCATGCTGACGG
GGAGAACGAAAGTGACAGGGTTCTCATAAAGTTGTATGAAATATCTCTACAAACCTCA
ATTAGTTCTACTCTACACTTCACTATCATCAACACTGAGACTATCCTGTCACCTACAAA
TGTGGAAACTTACATTGTTGATTTTCAGCAGACTTGTATTAAATTATTAGTG
TTAAGAATGCTAAATTATGTTCAATTCTATCTGTTATTGTACAA
CAAAGTAATAAGGATGGTTGTCAAAAAACAAACTATGCCTCTCTTTCAATCACC
AGTAGTATTTTGAGAAGACTGTGAACACTTAAGGAATGACTATTAAAGTCTTATTGTTA
TTTTTTCAAGGAAAGATGGATTCAAATAATTATTCTGTTTGCTTTAAAAAAA

FIGURE 112

MWLKVFTTFLSFATGACSGLKVTVPSPHTVHGVRGQALYLPVHYGFHTPASDIQIIWLFERPH
TMPKYLLGSVNKSVPDLEYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQGNGLTLSASQ
KIQVTVDPPVTKPVVQIHPPSGAVEYVGNTLTCHEGGTRLAYQWLKNGRPVHTSSTYSFS
PQNNTLHIAPVTKEDIGNYSCLVRNPVSEMESDIIMPIIYYGPYGLQVNNSDKGLKVGEVFTV
DLGEAILFDCSADSHPPNTYSWIRTDNTTYIIKGPRLEVASEKVAQKTMGYVCCAYNNIT
GRQDETHFTVIITSVGLEKLAQKGKSLPLASITGISLFLIISMCLLFLWKKYQPYKVIKQK
LEGRPETEYRKAQTFSGHEDALDDFGIYEFVAFPDVSGVSRIPSRSPASDCVSGQDLHSTV
YEVIQHIPAQQQDHPE

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 341-359

N-glycosylation site.

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,
276-280, 308-312

Casein kinase II phosphorylation site.

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

Tyrosine kinase phosphorylation site.

amino acids 272-280

N-myristoylation site.

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,
239-245

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 113

GCAAGCGCGAAATGGCGCCCTCCGGGAGTCTTGCAGTCTTCCCCTGGCAGTCCTGGTGTGTT
GCTTGGGGTGCTCCCTGGACGCACGGGGCGGAGCAACGTCGCGTCATCACGGACGAGA
ACTGGAGAGAACTGCTGGAAGGAGACTGGATGATAGAATTATGCCCGTGGTGCCTGCT
TGTCAAATCTCAACCGGAATGGGAAAGTTGCTGAATGGGAGAAGATCTGAGGTTAA
TATTGCGAAAGTAGATGTCACAGAGCAGCCAGGACTGAGTGGACGGTTATCATAACTGCTC
TTCCTACTATTATCATTGTAAGATGGTGAATTAGGCCTATCAGGGTCCAAGGACTAAG
AAGGACTTCATAAAACTTATAAGTGTAAAGAGTGGAAAGAGTATTGAGCCGTTCATCATG
GTTTGGTCCAGGTTCTGTTCTGATGAGTAGTATGTCAGCACTCTTCAGC**GTATCTATGTGGA**
TCAGGACGTGCCATAACTACTTATTGAAAGACCTGGATTGCCAGTGTGGGATCATATACT
GTTTTGCTTAGCAACTCTGTTCCGGACTGTTATTAGGACTCTGTATGATATTGTG
AGATTGCCTTGTCCTCAAAAAGCCGAGACCACAGCCATAACCCATAACCCCTCAAAAAAAAT
TATTATCAGAATCTGCACAACCTTGAAAAAAGTGGAGGAGGAACAAGAGGCGGATGAAGAA
GATGTTTCAGAAGAAGCTGAAAGTAAAGAAGGAACAAACAAAGACTTCCACAGAATGC
CATAAGACAAACGCTCTGGGTCCATCATTGCCACAGATAAATCCTAGTTAAATTTATAG
TTATCTTAATATTATGATTTGATAAAAACAGAACAGATTGATCATTGTTGGTTGAAGTG
AACTGTGACTTTTGAATATTGCAGGGTTCAGTCTAGATTGTCATTAAATTGAAGAGTCTA
CATTCAGAACATAAAAGCACTAGGTATACAAGTTGAAATATGATTAAGCACAGTATGATG
GTTAAATAGTTCTCTAATTTTGAAAAAATCGGCCAAGCAATAAGATTATGTATATTGT
TTAATAATAAACCTATTCAAGTCTGAGTTGAAAAATTTACATTCCCAAGTATTGCATTAT
TGAGGTATTAAAGAAGATTATTTTAGAGAAAAATATTCTCATTTGATATAATTTTCTG
TTCACTGTGTGAAAAAAAGAAGATATTCCATAAATGGGAAGTTGCCATTGTCTCAAG
AAATGTGTATTCAAGTACATTCGTGGCTTTAGAGGTATATTCCAAATTTCTTGT
ATTTTTAGGTTATGCAACTAATAAAACTACCTTACATTTAATTACAGTTCTACACA
TGGTAATACAGGATATGCTACTGATTTAGGAAGTTCATGGTATTCTCTTGATTC
CAACAAAGTTGATTTCTCTGATTTCTTACTTACTATGGGTACATTTTTATTTT
CAAATTGGATGATAATTCTTGGAAACATTTTATGTTTAGTAAACAGTATTTTGTT
GTTTCAAACTGAAGTTACTGAGAGATCCATCAAATTGAACAACTGTGTAATTAAAATT
TTGGCCACTTTTCAGATTTCATCATTCTTGTGAACTTCAACTGAAATTGTTT
TTTCTTTGGATGTGAAGGTGAACATTCTGATTTGTCTGATGTGAAAAAGCCTGGTA
TTTACATTGAAATTCAAAGAAGCTTAATATAAAAGTTGCATTACTCAGGAAAAAG
CATCTTCTTGATATGCTTAATGTATTTGTCCTCATATACAGAAAGTTCTTAATTGAT
TTTACAGTCTGTAATGCTGATGTTAAAATAAAACATTTTTATATTTTAAAAGACAA
ACTTCATATTATCCTGTTCTTCTGACTGGTAATATTGTGTGGGATTCCACAGGAAAAA
GTCAGTAGGATGGAACATTTTAGTGTATTTACTCCTTAAAGAGCTAGAATACATAGTTT
CACCTTAAAGAAGGGGAAATCATAAATACAATGAATCAACTGACCATTACGTAGTAGAC
AATTCTGTAATGTCCCCTCTTCTAGGCTCTGTTGCTGTGAATCCATTAGATTACAG
TATCGTAATACAGTTCTTAAAGCCCTCTCCTTAGAATTAAAATATTGTACCATT
AAAGAGTTGGATGTGTAACTTGTGATGCCTTAGAAAAATATCCTAAGCACAAAAAACCT
TTCTAACCACTCATTAAAGCTGAAAAAAAAAA

FIGURE 114

MAPSGSLAVPLAVLVLLWGAPWTHGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQNL
QPEWESFAEWGEDLEVNIAKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI
NFISDKEWKSIEPVSSWFGPGSVMSSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFAL
ATLFSGLLLGLCMIFVADCLCPSKRRRPQPYPPSKLLSESAQPLKKVEEEQEADEEDVSE
EEAESKEGTNKDFPQNPAIRQRSLGPSLATDKS

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 182-201

Casein kinase II phosphorylation site.

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

Tyrosine kinase phosphorylation site.

amino acids 107-115

N-myristoylation site.

amino acids 20-26, 192-198

Amidation site.

amino acids 25-29

FIGURE 115

GCGAGTGTCCAGCTGGGAGACCGTATAATTGTTAACTAATTCAACAAACGGGACCCCTT
CTGTGTGCCAGAAACCGCAAGCAGTTGCTAACCCAGTGGGACAGGCGGATTGGAAGAGCGGG
AAGGTCTGGCCCAGAGCAGTGTGACACTTCCTCTGTGACC**ATGAAACTCTGGGTGTCTGC**
ATTGCTGATGGCCTGGTTGGTGTCTGAGCTGTGTCAGGCCGATTCTCACCTTATTG
GGCACATGACTGACCTGATTATGCAGAGAAAGAGCTGGTGCAGTCTCTGAAAGAGTACATC
CTTGTGGAGGAAGCCAAGCTTCCAAGATTAAGAGCTGGCCAACAAAATGGAAGCCTTGAC
TAGCAAGTCAGCTGCTGATGCTGAGGGCTACCTGGCTCACCTGTGAATGCCAACAAACTGG
TGAAGCGCTAAACACAGACTGGCCTGGCTGGAGGACCTTGTCTGCAGGACTCAGCTGCA
GGTTTATGCCAACCTCTGTGAGCGGGCAGTTCTCCCCACTGATGAGGAGCAGAGATAGG
AGCTGCCAAAGCCCTGATGAGACTTCAGGACACATACAGGCTGGACCCAGGCACAATTCCA
GAGGGAACTTCCAGGAACCAAGTACCAAGGCAATGCTGAGTGTGGATGACTGCTTGGATG
GGCCGCTCGGCCTACAATGAAGGGACTATTATCATACGGTGTGATGGAGCAGGTGCT
AAAGCAGCTTGATGCCGGGAGGAGGCCACCACAACCAAGTCACAGGTGCTGGACTACCTCA
GCTATGCTGCTTCCAGTTGGGTGATCTGCACCGTGCCTGGAGCTCACCCGCCGCTGCTC
TCCCTGACCCAAGCCACGAACGAGCTGGAGGGATCTGGGTACTTTGAGCAGTTATTGGA
GGAAGAGAGAGAAAAACGTTAACAAATCAGACAGAAGCTGAGCTAGCAACCCAGAAGGCA
TCTATGAGAGGCCTGTGGACTACCTGCCTGAGAGGGATGTTACGAGAGCCTCTGCTGTGG
GAGGGTGTCAAACGTACACCCCCTAGACAGAAGAGGCTTTCTGTAGGTACCAACATGGCA
CAGGGCCCCACAGCTGCTCATTGCCCTCAAAGAGGAGGACGAGTGGGACAGCCCGACA
TCGTCAGGTACTACGATGTCATGTCATGAGGAAATCGAGAGGATCAAGGAGATCGCAAAA
CCTAAACTTGACGAGCCACCGTTGATCTGATCCAAAGACAGGAGTCTCACTGTCGCCAGCTA
CCGGTTTCAAAAGCTCCTGGCTAGAGGAAGATGATGACCCCTGTTGTGGCCCGAGTAAATC
GTCGGATGCAGCATATCACAGGGTTAACAGTAAAGACTGCAGAATTGTTACAGGTTGCAAAT
TATGGAGTGGGAGGACAGTATGAACCGACTTCGACTTCTAGGGCACCTTTGACAGCGG
CCTCAAAACAGAGGGAAATAGGTTAGCGACGTTCTTAACATGAGTGTAGAAGCTG
GTGGTGCACCGTCTCCCTGATCTGGGGCTGCAATTGGCTAAAGAAGGGTACAGCTGTG
TTCTGGTACAACCTCTGCGGAGCGGGGAAGGTGACTACCGAACAGACATGCTGCCG
TGTGCTTGTGGCTGCAAGTGGGTCTCCAATAAGTGGTCCATGAACGAGGACAGGAGTCT
TGAGACCTTGTGGATCAACAGAAGTTGACT**TGAC**ATCCTTCTGTCTTCCCTTGGTC
CTTCAGCCCAGTCAACGTGACAGACACCTTGTATGTTCTTGTATGTTCTATCAGGCT
GATTTTGGAGAAATGAATGTTGTCAGCGCCTAGCAAGGTGCCTTGTACCTCAGGTGTT
GTGACTGAAGTCCCAGCCCTCATTAGCCTGTGCCATCCCTGGCCCAAGGCTAGGATCA
AAGTGGCTGCAGCAGAGTTAGCTGTCTAGCGCCTAGCAAGGTGCCTTGTACCTCAGGTGTT
TTAGGTGTGAGATGTTCACTGAACCAAAGTTCTGATACCTTGTACATGTTGTTTAT
GGCATTCTATCTATTGTGGCTTACCAAAAAATAAAATGCTTACCAAGAAAAAA

FIGURE 116

MKLWVSALLMAWFGLSCVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVEEAKLSKIWSA
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALEDLVLQDSAAGFIANLSVQRQFFP
TDEDEIGAAKALMRLQDTYRLDPGTISRGELPGTKYQAMLSVDDCFGMGRSAYNEGYYHTV
LWMEQVLKQLDAGEEATTKSQVLDYLSYAVFQLGDLHRALELTRRLLSLDPHERAGGNLR
YFEQLLEEEREKTLTNQTEAELATPEGIYERPVDPYLPERDVYESLCRGEGVKLTPRRQKRLF
CRYHHGNRAPQLLIAPFKEEDEWDSPHIVRYVDVMSDEEIERIKEIAKPKLARATVRDPKTG
VLTVASYRVSKSSWLEEDDPVVARVNRRMQHITGLTVKTAELLQVANYVGQQYEPHFDFS
RRPFDSGLKTEGNRLATFLNYMSDVEAGGATVFPDLGAAIWPKKGTAVFWYNLLRSGEGDYR
TRHAACPVLVGCKWVSNKWFHERGQEFLRPCGSTEV

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 115-119, 264-268

Glycosaminoglycan attachment site.

amino acids 490-494

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 477-481

Casein kinase II phosphorylation site.

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,
346-350, 365-369, 385-389, 457-461, 530-534

Tyrosine kinase phosphorylation site.

amino acids 71-80, 489-496

N-myristoylation site.

amino acids 14-20, 131-137, 171-177, 446-452

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 8-19

Leucine zipper pattern.

amino acids 213-235

FIGURE 117

GCAGTATTGAGTTTACTCCCTCTTTAGTGGAGACAGACCATAATCCCAGTGTGAGTGAATTGATTGT
TTCATTATTACCGTTGGCTGGGGTAGTTCGACACCTTCAGTGAAGAGCAGGCAGAAGGGAGTTGTGA
AGACAGGACAATCTCTGGGATGCTGGCTCTGGAAAGCCAGCGGGCCTGCTCTGGCTTGGCTCATGACC
CAGGTTCTGGTAAAGCTACTACTGGCCTGGGCCATCAATCATTGATCCTTGAGGCTGTGCC
CCTGGGCACCCACCTGGCAGGGCTACCACCATGCACTGAGCTCCCTGTTGGCTCTGCTGCCAGCGCTTC
CCCTCATCTTAGGGCTGCTCTGGGCTGAGCCTGAGCCTGAGGGTTCCCTGGATCCAGGGGAGGGAGAAG
ATCCCTGTGTCGAGGCTGTAGGGAGCGAGGAGGGCACAGAACATCCAGATTGAGAGCTGGCTAGACCAAAGTG
ATGAAGACTTCAACCCCCGATTGTCCCCACTACAGGGACCCAACAAGCCCTACAAGAAGGTGCTCAGGACTC
GGTACATCCAGACAGAGCTGGCTCCCGTGAGCGTTGCTGGTGGCTGTCTGACCTCCGAGCTACACTGTCCA
CTTGGCCGTTGCTGTGAACCGTACGGTGGCCATCACITCCCTCGGTTACTCTACTCACTGGCAGGGGGGG
CCCGGGCTCCAGCAGGGATGCAAGGGTGTCTCATGGGATGAGCGGCCGCTGGCTCATGTCAGAGACCCCTGC
GCCACCTTCACACACACTTGGGCCACTACGACTGGTTCTCATCATGCAAGGATGACACATATGTGCAAGGCC
CCCGCTGGCAGGCCCTGCTGCCACCTCAGCATCAACCAAGACTGACTTAAAGGCGAGGAGTTCAATTG
GCGCAGGGCAGCAGGCCGTACTGTCAAGGGCTTGGCTACCTGTTGCTACGGAGTCTCTGCTTCGTGCTGC
GCCACATCTGGATGGCTGCCAGGGAGACATTCTCAGTGGCCGCTCTGACAGTGGCTTGGACGTCCTCATTTG
ACTCTCTGGCGTGGCTGTCTCACAGCACCCAGGGCAGCACTGCTCATTTGAACACTGGCAAAAATAGGG
ACCCCTGAGAAGGAAGGGAGCTGGCTTCTGAGTGCCTTCGCGTGCACCTGTCCTCGAAGGTACCCCTCATGT
ACCGGCTCCACAAACGCTCAGCGCTTGGAGTTGGAGCGGGCTTACAGTAAATAGAACAACTGCAAGGCTCAGA
TCCGAACTGACCGTGTGACCCCCCGAAGGGAGGCAGGGCTGAGCTGGCCGTTGGCTCCCTGCTCTTCA
CACCAACTCTGCTTGGAGGTGCTGGCTGGGACTACTTCACAGAGCAGCACACCTCTCCTGTCAGATGGGG
CTCCCAAGTGCCACTACAGGGGCTAGCAGGGCGACGTGGGTGATGCGTTGGAGACTGCCCTGGAGCAGCTCA
ATCGGCCTATCAGCCCCGCTCGCTTCCAGAAGCAGCGACTGTCACCGCTATCGCGCTTCGACCCAGCAC
GGGGCATGGAGTACACCTGGACCTGCTTGGAAATGTGTGACACAGCGTGGCAGGGCCCTGGCTCGCA
GGGTCACTGCTGCCACTGAGCCGGTGGAAATCTACCTATGCCCTATGTCAGTGGCCACCCGAGTGC
AGCTGGTGTGCCACTCTGGCTGAAGCTGCTGCAAGCCCCGGCTTCTCGAGGCGTTGCAAGCAATGTC
TGGAGCCACGAGAACATGCAATTGCTCACCTGTTGCTGAGTGGGCCACGAGAAGTGGCGTGGAGCTCCAG
ACCCATTCTGGGGTAGGGCTGCAGCAGCGAGTTAGAGCGACGGTACCCCTGGGACGAGGCTGGCTGGCTCG
CTGTGCGAGCAGAGGCCCTTCCCAGGTGCGACTCATGGACGTGGCTCGAAGAAGCACCCCTGTTGACACTCTCT
TCTTCCCTTACCAACCGTGTGGACAAGGCCCTGGGCCAGTCCCTAACCGCTGTCCTGACATGCAATTG
GGCAGGGCTTCTTCCAGTCCATTGGAGGTCAATCTGCGCTGTCACACAGAGTACCCCCAGGGCCCC
CGGGGGCTGGGCTGACCCCCCTCCCTGGCTGAGCTTCAACCGCTGTCACACAGAGTACCCCCAGGGCCCC
ACCCGGCAGGCTTCTGGGGAGGCTGCTTCAACACCGTCAACTCTGGCGCCGAGCCGGTGGCAGGTGAAC
TGGCAGGGCAGGAAGAGGAGGAAGGCCCTGGAGGGCTGGAGGTGATGGATTTTCTCCGGTTCTCAGGGCTCC
ACCTCTTCTGGGCCGTAGAGCAGGGCTGGTGCAGAAGTTCTCCCTGCGAGACTGCAAGCCCACGCTCAGTGAA
AACTCTACCAACCGCTGCCGCTCAGCAACCTGGAGGGCTAGGGGGCGTGGCCAGCTGGCTATGGCTCTTITG
AGCAGGAGCAGGCCAATAGCACTTAGCCGCTGGGGGCCCTAACCTCATACCTTCTGGTGTGCCCTCAGGCC
CCAGGAAGGGCAAGGAAGATGGGACAGATAGAGAATTGTTGCTGTATTAAATATGAAAATGTTATTAA
ACATGTCCTCTGCC

FIGURE 118

MRLSSLLALLRPALPLILGLSLGCSLSLLRVSWIQGEGEDPCVEAVGERGGPQNPDSRARLD
QSDEDFKPRIVPYYRDPNPKPYKKVLRTRYIQTTELGSRERLLVAVLTSRATLSTLAVAVNRTV
AHHFPRLLYFTGQRGARAPAGMQVVSQHDERPAWLMSETLRHLHTHFGADYDWFFIMQDDTY
VQAPRLAALAGHLSINQDLYLGRAEEFIGAGEQARYCHGGFGYLLRSLLLRLRPHLDGCRG
DILSARPDEWLGRCLIDSLGVGCVSQHQGQQYRSFELAKNRDPEKEGSSAFLSAFAVHPVSE
GTLMYRLHKRFSALELERAYSEIEQLQAQIRNLTVLTPEGAEAGLSPVGLPAPFTPNSRFEV
LGWDYFTEQHTFSCADGAPKCPLQGASRADVGALETALEQLNRRYQPRLRFQKQRLLNGYR
RFDPARGMETYLDLLLECUTQRGHRRALARRVSLRPLSRVEILPMPYVTEATRVQLVLPLL
VAEAAAAPAFLEAFAAANVLEPREHALLTLLVYGPREGGRGAPDPFLGVKAAAELERRYPG
TRLAWLAVRAEAPSQVRLMDVVSKKHPVDTLFFLTWTRPGPEVLNRCRMNAISGWQAFFP
VHFQEFPALSPQRSPGPPGAGPDPPSPGADPSRGAPIGGRFDQASAEGCFYNADYLAA
RARLAGELAGQEEEAELEGLEVMDVFLRFSGLHLFRAVEPGLVQKFSLRDCSPRLSEELYHR
CRLSNLEGLGGRAQLAMALFEQEANST

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 489-507

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-678

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 119

CGGAGTGGTGC~~G~~CCAA~~C~~GTGAGAGGAACCCGTGCGCGGCTGC~~G~~CTTCCTGTCCCCAAGCC
GTTCTAGACGCGGGAAAAATGCTTCTGAAAGCAGCTCCTTTGAAGGGTGTGATGCTTGG
AAGCATTCTGTGCTTGATCACTATGCTAGGACACATTAGGATTGGTATGGAAATAGAA
TGCACCACCATGAGCATCATCACCTACAAGCTCTAACAAAGAAGATATCTTGA~~AA~~ATTTC~~A~~
GAGGATGAGCGCATGGAGCTCAGTAAGAGCTTCGAGTATACTGTATTATCCTTGTAAAACC
CAAAGATGTGAGTCTTGGGCTGCAGTAAAGGAGACTGGACAAACACTGTGACAAAGCAG
AGTTCTCAGTTCTGAAAATGTTAAAGTGTGAGTCAATTAATATGGACACAAATGACATG
TGGTTAATGATGAGAAAAGCTTACAAATACGCCTTGATAAGTATAGAGACCAATACA~~A~~
GTTCTCCTTGCACGCCCACTACGTTGCTATCATTGAAAACCTAAAGTATTTTGTAA
AAAAGGATCCATCACAGCCTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATAT
GTGGGTATGGAAGGAGGAATTGTCTTAAGTGTAGAATCAATGAAAAGACTTAACAGCCTTCT
CAATATCCCAGAAAAGTGTCTGAACAGGGAGGGATGATTGGAAGATATCTGAAGATAAAC
AGCTAGCAGTTGCCTGAAATATGCTGGAGTATTGCAGAAAATGCAGAAGATGCTGATGGA
AAAGATGTATTAATACCAATCTGTTGGCTTCTATTAAAGAGGCAATGACTTATCACCC
CAACCAGGTAGTAGAAGGCTGTTGTCAGATATGGCTGTTACTTTAATGGACTGACTCCAA
ATCAGATGCATGTGATGTATGGGTATACGCCCTAGGGCATTGGCATATTTCAAT
GATGCATTGGTTTCTTACCTCAAATGGTCTGACAATGACTTGAGAAGTGGTAGAAAAGCG
TGAATATGATCTTGTATAGGACGTGTGTCATTATTGTAGTAGTA~~ACT~~ACATATCCAA
TACAGCTGTATGTTCTTTCTTAATTGGTGGCACTGGTATAACCACACATTAAAG
TCAGTAGTACATTTAAATGAGGGTGGTTTTCTTAAACACATGAACATTGAAATG
TGTGGAAAGAAGTGTAAAGAATAATAATTGCAAATAACTATTAAATAATTATAT
GTGATAAAATTCTAAATTATGAACATTAGAAATCTGTGGGCACATATTTGCTGATTGGTT
AAAAAATTAAACAGGTCTTAGCGTTCTAAGATATGCAAATGATATCTTAGTTGTGAATT
TGTGATTAAAGTAAAACCTTGTGTTCCCTTACTTCTAATACTGATTATGTTCT
AAGCCTCCCCAAGTCCAATGGATTGCCTCTCAAATGTACAACAGCAACTAAAGAAA
ATTAAAGTGAAGTTGAAAAAT

FIGURE 120

MLSSESSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERME
LSKSFRVYCIILVKPKDVSLWAAVKETWTKHCDKAEFFSSENVKFESINMDTNMDWLMMRK
AYKYAFDKYRDQYNWFFLARPTTFAIIENLKYFLLKKDPSQPFYLGHTIKSGDLEYVGMEGG
IVLSVESMKRLNSLLNIPEKCPEQGGMIWKISEDKQLAVCLKYAGVFAENAEDADGKDVFNT
KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGHIFNDALVFL
PPNGSDND

Signal sequence:

amino acids 1-33

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-672

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 121

CCACCGCGTCCGATCTTACCAACAAACACTCCTGAGGAGAAAGAAAGAGAGGGAGGGAGAG
AAAAAGAGAGAGAGAGAAACAAAAACCAAAGAGAGAGAAAAAATGAATTCATCTAAATCAT
CTGAAACACAATGCACAGAGAGAGGATGCTTCTCTTCCAAATGTTCTTATGGACTGTTGCT
GGGATCCCCATCCTATTCAGTGCCTGTTCATCACAGATGTGTTGACATTCGCAT
CTTCAAAACCTGTGATGAGAAAAGTTTAGCTACCTGAGAATTCACAGAGCTCTCCTGCT
ACAATTATGGATCAGGTTAGTCAAGAATTGTTGTCATTGAACTGGAAATATTCAAATCC
AGCTGCTACTCTTTCTACTGACACCATTCCCTGGCGTTAAGTTAAAGAACTGCTCAGC
CATGGGGCTCACCTGGTGGTTATCAACTCACAGGAGGAGCAGGAATTCCCTTCACAAGA
AACCTAAAATGAGAGAGTTTTATTGACTGTCAGACCAGGTTGTCAGGGTCAGGGCAA
TGGGTGGACGGCACACCTTGACAAAGTCTCTGAGCTCTGGATGTAGGGAGCCAAACAA
CATAGCTACCCTGGAGGACTGTGCCACCAGTGGAGACTCTCAAACCCAAGGCAAAATTGGA
ATGATGTAACCTGTTCTCAATTATTCGGATTGTGAAATGGTAGGAATAATCCTTG
AACAAAGGAAAATCTCTTTAAGAACAGAAGGCACAACCAAATGTGAAAGAAGGAAGAGCA
AGAACATGGCCACACCCACCGCCCCACACGAGAAATTGTCGCTGAACCTCAAAGGACTTC
ATAAGTATTGTTACTCTGATAAAATAAGTAGTTAAATGTTAAAAAAAAAAAAAAA
AAA
AAAAA

FIGURE 122

MNSSKSSETQCTERGCFSQMFLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPEN
FTELSCNYGSGSVKNCCPLNWEYFQSSCYFFSTDТИWALSLKNCSAMGAHLVVINSQEEQ
EFLSYKKPKMREFFIGLSDQVVEGQWQWVDGTPLTKSLSFWDVGEPPNNIATLEDCATMRDSS
NPRQNWNDVTCFLNYFRICEMVGINPLNKGS

Signal sequence:

amino acids 1-42

N-glycosylation site.

amino acids 2-6, 62-66, 107-111

Casein kinase II phosphorylation site.

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

N-myristoylation site.

amino acids 15-21, 74-80, 155-161

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 27-38

FIGURE 123

GGGACTACAAGCCGCCGCGCTGCCGCTGGCCCCCTCAGCAACCCTCGACATGGCGCTGAGGGGGCCACCGCG
TCCGGCTCTGCGCTCGGCTGCCGACTTCTTCCTGCTGCTGTTTCAGGGCTGCCTGATAGGGCTGAAATC
TCAAATCCAGCAATCGAACCCCAGTGGTACAGGAATTGAAAGTGTGGAACGTGCTGCATCATACGGATTGCG
AGACAAGTGACCCCAGGATCGAGTGGAAAGAAAATTCAAGATGAAACAAACACATATGTGTTTTGACAACAAAA
TTCAGGGAGACTTGGCGGGCTGTGCAGAAAATCTGGGAAAGACATCCCTGAAGATCTGGAATGTGACACGGAGAG
ACTCAGCCCTTATCGCTGTGAGGTGCTGCCAAGGAAATTGATGAGATTGTGATCGAGTTAA
CTGTGCAAGTGAAAGCCAGTGACCCCTGCTGTAGAGTGCGAAGGCTGTACCAAGTAGGCAAGATGGCAACACTG
ACTGCCAGGAGAGTGAGGGCCACCCCCGGCTCACTACAGCTGGTATCGCAATGATGTACCACTGCCACGGATT
CCAGAGCCAATCCCAGATTTCGCAATTCTCTTCACTTAAACTCTGAAACAGGCACCTTGGTGTCACTGCTG
TTCACAAGGACGACTCTGGCAGTACTACTGCATTGCTTCAATGACGCAAGGCTCAGCCAGGTGAGGAGCAGG
AGATGGAAGTCTATGACCTGAACATTGGCGGAATTATTGGGGGGTTCTGGTGTCTGCTGACTGCCCTG
TCACGTTGGGACTGCTGTGCATACAGACGTGGCTACTTCATCAACAATAACAGGATGGAGAAAGTTACAAGA
ACCCAGGGAAACCAAGATGGAGTTAACTACATCCGACTGACGAGGAGGGGACTTCAGACACAAGTCATCGTTG
TGATCTGAACCCCGGGTGTGGCTGAGAGCGCACAGAGCAGTCACATACCTCTGCTAGAAAACCTCTGCTCAA
GGCAGCGAGAGCTGATGCACTCGGACAGAGCTAGACACTCATCAGAAGCTTCTGGCTTGGCCAAGGTTGACCA
CTACTCTCTTAACAAAGCCACATGAATAGAAGAATTTCCTCAAGATGGACCCGGTAAATATAACCACAA
GGAAGCGAAACTGGGTGCGTCACTGAGTTGGGTTCTAACTGTGTTCTGGCTGATTCCCGCATGAGTATTAGG
GTGATCTTAAAGAGTTGCTACGTAACGCCGTCGAGATGGCGAGGGTGGCTGAGCAGCACAGCAGCGCATCCGG
CAGCAGCCACGACAGCACCATGTGAGATGGCGAGGGTGGCTGAGCAGCACAGCAGCGCATCCGGCGGGAAACCA
GAAAGGCTTCTTACACAGCAGCCTTACTTCATCGGCCCACAGACACCACCGCAGTTCTTAAAGGCTCTGC
TGATCGGGTGTGCACTGTCATTGAGGCTTGTGAAAGCTTGTGAAAGCTTGTGAAAGCTTGTGAAAGCTTGTG
GTAAATTGGTTGCTGGAGAGGGATCTTGCCTGAGGAACCTGCTTGTCCAACAGGGTGTCACTGGGTTAAGGAAA
ACCTTGTCTTAGGCTAAGTGTGAAATGGTACTGAAATATGCTTTCTATGGGTCTTGTGTTATTGTTATAAAATT
TACATCTAAATTGCTAAGGATGTATTGATTGAAAGAATTCTATTAAACTGTAATATATTGT
CATACAACTGTTAAATAACCTATTGTTAAAGGCTTCAACTTAAGGTTAGAAGTCTAACGCTACTAGTGTG
TGGAAAATATCAATAATTAAAGAGTATTGTTACCCAAGGAATCCTCTCATGAAAGTTACTGTGATGTTCTTTCT
CACACAAGTTAGCCTTTTCAAAAGGAACCTCATACTGTCTCACATGACCATAGTGTCTAGGAAACCTT
TAAAATCCAGTTAAGCAATGTTGAAATCAGTTGCTCATCTTCAAAAGAAACCTCTCAGGTTGACTTTGAAC
GCCTCTCTGAGATGACTAGGACAGTCGTACCCAGAGGCCACCCAGAACGCCCTCAGATGATACACAGATG
CCAGTCAGCTCCTGGGGTTGCCAGGGCCCCCTAGCTACTGTTGCTCGCTGTCTGCCAGGAGGCC
GCCATCCTGGGCCCTGGCAGTGGCTGTGCTCCAGTGTGAGCTTACTCAGTGGCCCTTGCTTCACTCAGCAG
TCTCAGGTTGGCACTGCAGGGACACTGGTGTCTTCCATGTAGCGTCCCAGCTTGGCTCTGTAAACAGACCT
TTTGGTTATGGATGGCTCACAAAATAGGGCCCCAATGCTATTGTTAAAGTTGTTAATTATTGTT
AACATTGTCTAAGGCCAAAGGCAATTGCAAATCAAGTCTGTCAGTACAATAACATTGTTAAAGAAAATGGAT
CCCACTGTTCTCTTGCCACAGAGAAAGCACCCAGACGCCACAGGCTCTGCGATTCAAAACAAACCATGAT
GGAGTGGCGGCCAGTCCAGCCTTTAAAGAACGTCAAGGTGGAGCAGCCAGGTGAAAGGCTGGGGGGAGGAAAG
TGAAACGCCCTGAATCAAAGCAGTTCTAATTGACTTTAATTGTTCATCCGCCAGACACTGCTCCATT
TGTGGGGGGACATTAGCAACATCACTCAGAAGCCTGTTCTCAAGAGCAGGTGTTCTCAGCCTCACATGCCCT
GCCGCTGCTGGACTCAGGACTGAAAGCTGCTGAAAGCAAGGAGCTGCTGAGAAGGAGCACTCCACTGTGCTGCC
GAATGGCTCTCACTACTCACCTGTCTTCAGCTTCCAGTGTCTTGGGTTTTTATACATTGACAGCTTTTT
AATTGCTACATGAGACTGTGTTGACTTTTGTGAAACACTTGCCTACAGCTGAGACTAG
GGAAATGCTCCAGCAGTGGCTCAGTGTCTCCCTGGTCTGCTGCATGGCATCTGGATGCTTAGCATGCAAGGTC
CCTCCATCATGGCCACCTGGTAGAGAGGGATGGCTCCACCCCTCAGCGTTGGGATTCTACGCTCCAGGCC
TCTTGGTTGTCATAGTGTAGGGTAGCCTTATTGCCCCCTTCTTCTATACCTAAACCTTCTACACTAGTGC
TGGGAACCAAGGTGCAAAAGTAGAGAGAACGTGAAAGTAGAGTCTGGGAAAGTAGCTGCCCTATAACTGAGACTAGA
CGGAAAAGGAATACTCGTGTATTGTTAAGATGAAATGTGACTCAAGACTCGAGGCCGATACGAGGCTGTGATTCT
GCCTTGGATGGATGTTGCTGTACACAGATGCTACAGACTGTACTAACACACCGTAATTGGCATTGTTAAC
CTCATATAAAAGCTCAAAAAACCCCA

FIGURE 124

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624
><subunit 1 of 1, 310 aa, 1 stop
><MW: 35020, pI: 7.90, NX(S/T): 3
MALRRPPRLRLCARLPDFLFFFRLGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTSD
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVVARNDRK
EIDEIVIELTVQVKPVTVPVCRVPKAVPGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDLDLNIGGIIGG
VLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI
```

Important features of the protein:

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 243-263

N-glycosylation sites.

amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-110

Casein kinase II phosphorylation site.

amino acids 106-109, 296-299

Tyrosine kinase phosphorylation site.

amino acids 69-77

N-myristoylation sites.

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267